```
; Search time 98 Seconds (without alignments) 530.773 Million cell updates/sec
                                                                                                                                                                                                                       1 MGCGGSRADAIEPRYYESWT......VTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                         2002273
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  2002273 seqs, 358729299 residues
                                                                                                             November 17, 2004, 14:58:39
                                                                        using sw model
                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                 US-10-705-716A-4
                                                                        - protein search,
                 Copyright
                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                              Scoring table:
                                                                          OM protein
                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                             Run on:
```

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 23Sep04:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aab95018 Human pro Aac19498 HSI prote Abz58646 Human can Adc31800 Human nov Adm46959 Brain and Adc48475 Human PTH Adc48479 House PTH Adc48479 Mouse PTH Adc48479 Rat PTH r Adc48479 Rat pTH r Adc48470 Human dio Adc48477 Human PTH Adc48477 Human PTH Adc48477 Human PTH Adc48471 Human PTH Adc48481 Mouse PTH Adc48481 Acabidops Acu15389 Arabidops
SUMMARIES	AAB95018 AAC19498 AAC19498 AAC131800 ADM46959 ADC48475 ADM468473 ADC48473 ADC48473 ADC48477 ADM46960 ADC48477 ADM46960 ADC484877 ADM46979 ADM46979 ADM46979 ADM46979 AAC15390 AAC15390 AAC15390 AAC15389 AAC1629 AAC1629 AAC1629
DB	450077878875777878775567
* Query Match Length	145 145 145 145 145 145 145 145 145 145
% Query Match	1000.0 10000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1
Score	77.8 77.8
Result No.	

Aab80297 Human pro Abr4815 Human bla Abu56516 Lung canc Abo58424 Human gen Abg02038 Novel hum Adm87821 Human EST Abg09910 Novel hum Abb04711 Human FST	Aab83195 Human Rec Ado55153 Protein # Abu34190 Protein e Aao17108 Murine Gl	Aag81103 Mycobacte Abb659310 Drosophil Abb65489 Drosophil Abb65488 Drosophil	Abb65280 Drosophil Abg14111 Novel hum Aab59813 TutD prot Aab59826 Protein #
AABB0297 ABR4 8215 ABU5 6516 ABC5 8424 ABG02038 ADM87 821 ABG09910	AAB83195 ADO55153 ABU34190 AAO17108	AAG81103 ABB69330 ABB65489 ABB65488	ABB65280 ABG14111 AAB59813 AAB59826
4 4 6 8 4 8 4 10	4800	4444	4444
369 369 369 383 1192 508 508	991 991 486 1111	514 684 899 899	659 547 1017 1615
11.2	1.11.	10.8 10.7 10.7 10.7	10.7 10.6 10.6 10.6
87.5 87.5 87.5 86.5 86	86 86 85 85	83.5 83.5 83.5	82.5 82.5 82.5
9 7 8 8 7 8 8 7 8 8 9 8 9 8 9 9 8 9 9 8 9 9 8 9 9 9 9	36 36 36 7	38 39 44 11	4 4 4 4 2 6 4 3

## ALIGNMENTS

```
Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                    Human protein sequence SEQ ID NO:16726.
             AAB95018 standard; protein; 145 AA
                                                                                                                                    29-JUL-1999; 99JP-00248036.
27-AuG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00187767.
09-JUN-2000; 2000JP-002418999.
                                                                                                                        28-JUL-2000; 2000EP-00116126.
                                       (first entry)
                                                                                                                                                                             (HELI-) HELIX RES INST
                                                                                Homo sapiens.
                                                                                             EP1074617-A2.
                                                                                                           07-FEB-2001.
                                        26-JUN-2001
                          AAB95018;
RESULT 1
     AAB95018
```

Yamamoto J; Saito K, Ya , Otsuki T; Isogai T, Nishikawa T, Hayashi K, Si , Sugiyama T, Wakamatsu A, Nagai K, Ota T, IE Ishii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 8; SEQ ID NO 16726; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

us-10-705-716a-4.rag

```
ô
sequence and an oligonucleotide comprising a sequence complementary to a polymucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers can be used in antisense therapy and in particularly full-length cDNas. The primers are useful for synthesising polynucleotides, particularly full-length cDNas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNas. The primers allow obtaining of the full-length cDNas easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13621 represent human amino acid sequences; and AAH13629 to AAH3621 represent colligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                            PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS1; variant; cancer; tumour; unigene cluster; cytostatic; metastasis; EST; expressed sequence tag; colon cancer; stomach cancer; breast cancer; HS169395; HS127144; HS2; HS132793; HS3.
                                                                                                                                                                                                                                                                                                                                                                                          PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                   Length 145;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                   Score 778; DB 4;
Pred. No. 3.8e-70;
                                                                                                                                                                                                                                                   100.0%; Scor.
100.0%; Pred. No. s..
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVIINVIDSIQOMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVTINVTDSIQOMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA019498 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2001; 2001DE-01003694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2001; 2001DE-01003694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                               Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS1 protein variant
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                        present invention
                                                                                                                                                                                                                                     Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE10103694-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA019498;
                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA019498
      ^{\circ}
                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                             ⋧
                                                                                                                                                                                                                                                                                                                                                                                        ਨੇ
```

```
o
o
                                                                                                                                                                                                                                                                                                                                     PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                    PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-
                                                                                         solid
                                                                                                                                                                                                                                                                     1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genes that are up-regulated or down-regulated in cancers, useful markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                       Gaps
                      lymph nodes are
(HS2) and/or HS132793 (HS3) for diagnosis and therapy of tumours, which their expression rates in tumour cells and/or lymph nodes ar determined. The EST sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with adevelopment of metasrases); and for diagnosis and/or therapy of so tumours, particularly of colon, stomach and breast. The present seins a variant of the HS1 protein shown in the exemplification of the invention
                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                    Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson KE;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                    100.0%; Score 778; DB 5;
100.0%; Pred. No. 3.8e-70;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer related protein SEQ ID NO:303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hevezi PA,
                                                                                                                                                                                                                                                                                                                                                                                                 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                 EVTINVIDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR58646 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 753; 767pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-2001; 2001US-0323469P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2002; 2002US-0355145P
08-FEB-2002; 2002US-0355257P
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-2002; 2002WO-US029560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gish KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                      Best_Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-354600/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACC72796
                                                                                                                                                                       Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003025138-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR58646;
                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Afar D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR58646
      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

determining expression rates of the unigene cluster, and subsequently

φğ

Diagnosis and therapy of tumors, specific expressed sequence tags

WPI; 2002-644836/70. N-PSDB; AAL50100. Brett D, Kemmner W;

blocking their expression.

Claim 10; Page 5; 10pp; German.

(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

The present invention relates to the use of expressed sequence tags (ESTs), or variants, of the unigene cluster HS169395 (HS1), HS127144

```
regulated in specific cancers (e.g. about 1031 genes up-regulated in caute lymphocytic leukemia). ACC72641 to ACC72660 represent cancer related gene mucleotide sequences which encode the proteins given in ARR58721 to ARR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a cherapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in a charm screening, particularly for identifying agents for treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 778; DB 6; Length 145; 100.0%; Pred. No. 3.8e-70; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human novel polypeptide sequence, SEQ ID NO:1882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xue AJ, Zhao QA,
Ma Y, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC31800 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; chromosome 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003029271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                              pathologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC31800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

Wehrman T;

Wang J, Wang Z,

Weng G;

Tang TY, Zhang J, Ren F, Xue AJ, Zhou P, Ghosh M, Wang D, Ma Y, A Haley-Vicente D, Drmanac RT;

```
The invention relates to 971 novel human cDNA sequences (ADC29919-ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to muclaic acid sequences over 99; identical with chroation also relates to muclaic acid sequences over 99; identical with invention also relates to muclaic acid sequences over 99; identical with crower board and a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of cidentifying a compound which binds to a polypeptide of the invention; and methods of invention further discloss methods of peventing, treating or ameliorating a medical condition; kits comprising polymucleotide probes and/or monotonal antibodies for carrying out the methods of the invention conting a medical condition; kits comprising polymucleotide probes and/or monotonal antibodies for carrying out the methods of the invention conting sequences corresponding to the cDNA sequences of the invention conting sequences corresponding to the cDNA sequences of the invention are expression or activity of the polymelede and/or polypeptide; and 767 conting sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the cheful in diagnostics, drug screening, forensics, gene mapping, in the dentification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are disease and other neurodegenerative diseases, anaemia, platelet concer. The nucleic acids may also be used as hybridisation products of sequence represents a specifically claimed human polypeptides sequence represents a specifically claimed human polypeptides equence of the invention. Note: The sequence of the invention. Note: The sequence of the polymel of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                               New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PSNGVPRSTAPGGIPNPEXKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brain and Acute Leukemia, Cytoplasmic alternate protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acute myelogenous leukemia; gene expression; BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 778; DB 7;
100.0%; Pred. No. 3.8e-70;
ive 0; Mismatches 0;
                                                                                                                                                                                          Claim 20; SEQ ID NO 1882; 1185pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EVIINVIDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM46959 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 145; Conservative
2003-371981/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                 N-PSDB; ADC30829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM46959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #X#X#X#X#
##X#####X#X99999999999999999999999999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 βp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

```
leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                               in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of characterizing acute myelogenous
                                                                                                                                                                                                                                                                                                                                                                                                               Characterizing acute or chronic myelogenous leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 17; 78pp; English
                                                                                                                       /note= "encoded by GCS"
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                         (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                         09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                         12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                             De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-441564/41.
                   Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADM46951
                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 145 AA;
                                                                                                                                                       WO2003040347-A2.
                                                     Homo sapiens
                                                                                                                                                                                         15-MAY-2003
                                                                                                                                                                                                                                                                                                                             Tanner SM,
```

invention relates to a novel PTH responsive gene (PAIGB) fragment

Claim 9; SEQ ID NO 4; 169pp; English.

New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.

Murrills RJ;

Stojanovic-Susulic V, Babij P,

WPI; 2004-420299/39 N-PSDB; ADO48474

(AMHP ) WYETH Robinson JA,

10-NOV-2003; 2003WO-US035655 12-NOV-2002; 2002US-0425532P

WO2004044152-A2.

27-MAY-2004

```
construct comprising the isolated nucleic acid fragment operatively characterized a solated nucleic acid fragment of the nucleic acid fragment obtaining a polypeptide, detecting the pulse construct, a wector comprising the nucleic acid fragment, obtaining a polypeptide, detecting the presence of the nucleic acid fragment an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide, a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide, careflectiveness in altering expression of the nucleic acid fragment; screening spent alters the expression of PAIGB mRNA, careflectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders, evaluating for agents useful for treating bone related disorders; and subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a bone related disorders in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a bone related disorders acmposed of the transgenic animal and a second group of animals; studying bone mass determinants; studying the modulation of bone mass; studying bone related disorders; identifying where an activity and a stephy transfected cell line comprising two constructs, the first construct comprising a ligand binding domain of linked to a DNA binding domain which is linked to an activation domain can infinal promoter which is linked to PAIGB cDNA, where promoter, the second construct comprising multiple opies of DNA binding elements linked to a part the partition of partitions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in
PSNGVPRSTAPGGI PNPEKKTNCETOCPNPOSLSSGPLTOKONGLOTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 778; DB 7; Length 145; 100.0%; Pred. No. 3.8e-70; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVIINVIDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 BVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO48475 standard; protein; 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO48475
```

g

ద

8 g

ਨੋ

```
ö
                                                                                                                                                                                                                                                                                                                                                 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                 9
preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH
                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                        PSNGVPRSTAPGGI PNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                                                                                                        Gaps
                                                                                                                                                                                     ..
0
                                                                                                                                          Length 145;
                                                                                                                                                                                   Indels
                                                                                                     100.0%; Score 778; DB e, Pred. No. 3.8e-70;
                        related disorders, e.g., osteoporosis. The responsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  121 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 145; Conservative
                                                                                            Sequence 145 AA;
                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                  셤
```

PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; human.

Homo sapiens.

Human PTH responsive gene protein.

SXXXXXXXXXXXXXXXX

12-AUG-2004 (first entry)

```
121
```

Brain and Acute Leukemia, Cytoplasmic alternate protein #3 ADM46961 standard; protein; 180 AA (first entry) Cytoplasmic, exon. 03-JUN-2004 ADM46961; chronic ADM46961 

myelogenous leukemia; gene expression; BAALC; ic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

Homo sapiens

Location/Qualifiers Key Misc-difference

'note= "encoded by GCS"

WO2003040347-A2.

15-MAY-2003

12-NOV-2002; 2002WO-US036375.

09-NOV-2001; 2001US-0348210P.

(OHIS ) UNIV OHIO STATE RES FOUND.

De La Chapell A; Tanner SM,

WPI; 2003-441564/41.

N-PSDB; ADM46953

Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.

Disclosure; SEQ ID NO 19; 78pp; English

The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAMLC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAMLC overexpression. This sequence corresponds to a BAMLC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.

Sequence 180 AA;

```
61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                           QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                               121 QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 180
                                                                                                      9
                                                                                                                                          -----GMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 85
                                                                      53
                                                                                           MGCGGSRADAI EPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS----
                                     35;
96.5%; Score 750.5; DB 7; Length 180; 80.6%; Pred. No. 3e-67; ive 0; Mismatches 0; Indels 35.
                                   Conservative
                Local Similarity
                     3est Local Simi
fatches 145;
                                                                      Н
                                                                                                                                        54
 Query Match
                                                                      ð
                                                                                                 d
                                                                                                                                      ò
                                                                                                                                                                     g
                                                                                                                                                                                                           à
```

ADO48479 standard; protein; 145 AA. RESULT 8 ADO48479 

ADO48479:

(first entry) 12-AUG-2004

Mouse PTH responsive gene protein.

PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; mouse; murine

Mus sp

WO2004044152-A2.

27-MAY-2004.

10-NOV-2003; 2003WO-US035655.

12-NOV-2002; 2002US-0425532P.

(AMHP ) WYETH

Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ;

WPI; 2004-420299/39.

New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. N-PSDB; AD048478

Claim 9; SEQ ID NO 8; 169pp; English.

The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively in the isolated nucleic acid fragment operatively clinked to suitable regulatory sequences; a host cell transformed with the chaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a nucleic acid fragment the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; cereening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a bone evaluating the effectiveness of treatment of a bone forming to PAIGB; monitoring the effectiveness of treatment of a bone forming to PAIGB; monitoring the effectiveness of treatment of a bone evaluating to the paid to related agent; a transgenic animal comprising the DNA; an animal model

for the study of bone density modulation comprising a first group of
animals composed of the transgenic animal and a second group of
animals composed of the transgenic animal and a second group of
animals; studying bone mass determinants; studying the modulation of bone
composed of the state of the state of the state of the modulation of the
composed of the state of the st

```
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM46963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM46963
  8888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the linked to suitable regulatory sequences; a host cell transformed with the chaining a nucleic acid fragment encoding the polypeptide; amethod for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of ragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody determining whether an agent atters the expression of PAIGB gene or polypeptide; acreening agents for effectiveness in altering expression of the nucleic acid fragment, screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related clisorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone
                                                                   ö
                                                                                                                                                              PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                             09
                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                            PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; rat.
                                                                                                           1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid fragment encoding a PAIGB polypeptide, useful in
preparing a composition for diagnosing, treating or preventing bone
                                                                   .
0
                                         Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murrills RJ;
                                                                 14; Indels
                                      Query Match 83.4%; Score 649; DB 8; Best Local Similarity 83.4%; Pred. No. 3.8e-57; Matches 121; Conservative 10; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babij P,
                                                                                                                                                                                                               EVIINVIDSIQOMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preparing a composition for diagnosing related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID NO 2; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robinson JA, Stojanovic-Susulic V,
                                                                                                                                                                                                                                                                                        ADO48473 standard; protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                      Rat PTH responsive gene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                            12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-420299/39.
                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADO48472.
             Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004044152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                                                                                                   ADO48473;
                                                                                                                                              61
                                                                                                                                                                                                121
                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                             ADO48473
XX OS
                                                                                                                  g
                                                                                                                                                                      g
                                                                                                                                                                                                ð
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                  ð
```

```
correlated agent; a transgenic animal comportaing the DNA; an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone carriers of the starting bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain of linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a ninimal promoter which is linked to PAIGB Sune is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be composition for diagnosing, treating or preventing bone related disorders, e.g., osteoprossis. This sequence represents a PTH creptonsive gene party.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSNGVLRPAAPGGIANPEKKANCGTQCPNSQSLSSGPLTQKQNGLWTTEAKKDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acute myelogenous leukemia; gene expression; BAALC;
chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.9%; Score 645; DB 8; Length 145; Best Local Similarity 83.4%; Pred. No. 9.6e-57; Matches 121; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brain and Acute Leukemia, Cytoplasmic alternate protein #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || |:||:||:||||:|
121 EVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM46963 standard; protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L2-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanner SM, De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-441564/41.
N-PSDB; ADM46955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003040347-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2003.
```

```
The invention relates to a method of characterizing acute myelogenous leukemia (AMI) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AMI. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                             Disclosure; SEQ ID NO 21; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 149 AA;
```

61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIFNPEKKTNCET 120 23 9 85 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS -----GMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET Gaps 35; MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS-Length 149; Indels DB 7; ; 0 Score 569.5; DB Pred. No. 4e-49; 0; Mismatches 144 QCPNPQSLSSGPLTQKQNGLQTTE 109 QCPNPQSLSSGPLTQKQNGLQTTE 73.28; Conservative Similarity 109; н Query Match 86 121 Local Matches 임 g 셤 δ ò

ADQ81902 standard; protein; 92 09-SEP-2004 (first entry) Human dioxygenase 10.12 ADQ81902; ADQ81902 

Ą

Human; enzyme; dioxygenase 10.12; malignant tumour; inflammation; immunological disease; haemopathy; HIV infection.

Homo sapiens.

CN1344798-A. 17-APR-2002. 29-SEP-2000; 2000CN-00125495.

29-SEP-2000; 2000CN-00125495

(SHAN-) SHANGHAI BIODOOR GENE DEV CO LID.

Mao Y,

WPI; 2002-509506/55. N-PSDB; ADQ81901. New polypeptide human dioxygenase 10.12 and polynucleotides encoding this polypeptide, useful for treating various diseases, such as malignant tumors, inflammations, immunological diseases, hemopathy and HIV infection.

Claim 1; SEQ ID NO 2; 33pp; Chinese.

The present invention discloses a new kind of polypeptide, human

```
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Characterizing acute or chronic myelogenous leukemia, or prostate cancer
dioxygenase 10.12, polynuclectides encoding this polypeptide, a DNA recombination process to produce the polypeptide and antagonist against the polypeptide. The present invention also discloses the method of applying the polypeptide in treating various diseases, such as malignant tumours, inflammations, immunological diseases, haemopathy and HIV infection. The present sequence is the human dioxygenase 10.12.
                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                   -----NAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNG
                                                                                                                                                                                                                                45 GPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNG
                                                                                                                                                                                               Gaps
                                                                                                                                                                                               19;
                                                                                                                                                           Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain and Acute Leukemia, Cytoplasmic alternate protein #4.
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                    105 LQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                       52 LOTTEAKRDAKRMPAKEVTINVTDSIQOMDRSRRITKNCVN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myelogenous leukemia; gene expression; BAALC;
                                                                                                                                                             DB 5;
                                                                                                                                                           52.1%; Score 405.5; DB 5; 79.2%; Pred. No. 7.2e-33; iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 20; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADM46962 standard; protein; 73 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-441564/41.
                                                                                                                                                                               Local Similarity
hes 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic; exon.
                                                                                                                                                                                                                                                                     11 GPETG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADM46954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003040347-A2
                                                                                                                              A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-2004
                                                                                                                              Sequence 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanner SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM46962;
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acute
                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                ADM46962
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8888888888
                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                       엄
```

Ź

ADO48477 standard; protein; 54

ADO48477

(first entry)

12-AUG-2004 ADO48477;

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods kits and probes are useful for characterizing acute or Theoric myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                        myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLED 58
                                                                                                           1 MGCGCSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of characterizing acute myelogenous
                                                              Gaps
                                                              ..
                                                                                                                                                                                                                                                                                        Brain and Acute Leukemia, Cytoplasmic alternate protein #2
                                Length 73;
                                                            1; Indels
                                                                                                                                                                                                                                                                                                                      acute myelogenous leukemia; gene expression; BAALC;
                              Score 309; DB 7;
Pred. No. 2.8e-23;
.; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.4%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 18; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                    Ź
                                                                                                                                                                                              ADM46960 standard; protein; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-2002; 2002WO-US036375.
                              39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De La Chapell A;
                                                                                                                                                                                                                                                            (first entry)
                                                         56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-441564/41.
                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADM46952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003040347-A2
Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54 AA;
                                                                                                                                                                                                                                                            03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanner SM,
                                                                                                                                                                                                                              ADM46960;
                                                                                                                                                                                                                                                                                                                                         chronic
                                                         Matches
                                                                                                                                                                                   ADM46960
S
                                                                                                                                                                                                                            ò
```

```
The invention relates to a novel PTH responsive gene (PAIGB) fragment concluding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively construct comprising the isolated nucleic acid fragment operatively interest construct; a vector comprising the nucleic acid fragment; containing a polypeptide; a detecting the presence of the nucleic acid obtaining a nucleic acid fragment encoding the polypeptide; a method for cobtaining a polypeptide; a composition for regulating bone-forming activity of rangment an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity of a mammal comprising the nucleic acid fragment, polypeptide; a composition for regulating bone-forming activity of a resenting agents the expression of PAIGB mRNA; an agent that alters the expression of PAIGB mRNA; screening the effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorder in a subject; identifying polypeptides capable of binding to acid fragment; screening for agents useful for treatment of a bone related disorder; an authoring the effectiveness of treatment of a subject with a bone control and accord group of control animals composed of the transgenic animal comprising the DNA; an animal model for the study of bone density modulation comprising a first group of control animals; studying an effect of PAIGB on bone disorders; identifying an effect of FAIGB on bone disorders; identifying whether an agent which has bone forming activity, and a stably transfected cell linked to a DNA binding domain which is linked to an activation domain which has bone forming activity, and a stably where upon the addition animal producer, transcribing multiple copies of DNA binding elements linke to a minimal promoter which is linked to an activation and activity, and a composition of PAIGB only where upon the addition cofference and construct com
                                                                                                                                                                 bone density modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.
                                                                                                                                                        PTH responsive gene; PAIGB; bone-forming; bone; bone density modul transgenic animal; osteopathic; gene therapy; osteoporosis; human.
                                                                                                                 Human PTH responsive gene protein exon 2 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stojanovic-Susulic V, Babij P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 6; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                       10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                   L2-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-420299/39.
N-PSDB; ADO48476.
                                                                                                                                                                                                                                                                            WO2004044152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMHP ) WYETH
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robinson JA,
```

Sequence 54 AA;

ö

Gaps

ö

0; Indels

Length 54;

Score 299; DB 7; I Pred. No. 1.9e-22;

Conservative

54;

à g

Similarity

Local Matches

Query Match

54

1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG

Job time : 101 secs

ö

```
The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                              acute myelogenous leukemia; gene expression; BAALC;
chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                    Gaps
                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54
                                                                    1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54
                                    ..
                                                                                                                                                                                                                                                                                               Brain and Acute Leukemia, Cytoplasmic alternate protein #6.
Query Match 38.4%; Score 299; DB 8; Length 54; Best Local Similarity 100.0%; Pred. No. 1.9e-22; Matches 54; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 22; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                          ADM46964 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-2002; 2002WO-US036375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De La Chapell A;
                                                                                                                                                                                                                                                                 03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-441564/41.
N-PSDB; ADM46956.
                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003040347-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fanner SM,
                                                                                                                                                                                                                                ADM46964;
                                                                                                                                                           RESULT 15
ADM46964
                                                                                                                                                                                              ò
                                                                                                       셤
```

Gaps . 0 37.7%; Score 293; DB 7; Length 80; 100.0%; Pred. No. 1.3e-21; cive 0; Mismatches 0; Indels Ouery Match
Best Local Similarity 100.
Matches 53; Conservative

Sequence 80 AA;

; 0

1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS 53

à 셤 Search completed: November 17, 2004, 15:22:24

Н

Sequence 149, App Sequence 32058, A Sequence 340590, Sequence 179100, Sequence 179100, A Sequence 134726, A Sequence 12110, A Sequence 12110, A Sequence 154, App Sequence 17910, App

Searched:

Database

Sequence:

```
DEBLEAL TROUGHTS. Temper, Stephan APPLICANT: Tanner, Stephan APPLICANT: Tanner, Stephan APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BABLC expression as a diagnostic marker for acute leukemia FITLE OF INVENTION: BABLC expression as a diagnostic marker for acute leukemia FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIBPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 778; DB 14; Length 145; Best Local Similarity 100.0%; Pred. No. 1.4e-66; Matches 145; Conservative 0; Mismatches 0; Indels 0.
4 US-10-910-600-26

4 US-10-136-822-84

5 US-10-188-832-189

7 US-10-029-386-32058

7 US-10-425-115-340590

5 US-10-425-114-7799

5 US-10-425-114-7799

6 US-10-425-114-7799

10S-10-425-114-71015

5 US-10-425-114-7799

10S-10-425-114-7910

10S-10-425-114-7910

10S-10-427-363-158

10S-10-427-363-158

10S-10-437-963-15852

10S-10-437-963-15852

10S-10-437-963-15852

10S-10-437-963-15852

10S-10-437-963-15852

10S-10-437-963-15852

10S-10-437-963-15852

10S-10-437-963-15852

10S-10-437-963-163549

10S-10-437-963-163549

10S-10-437-963-163549

10S-10-437-963-163549

10S-10-425-114-69355

10S-10-423-363-107997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-269-390-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVIINVIDSIQOMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-293-239-17
, Sequence 17, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
    US-10-293-239-17
                                                                                                                                                                                                        85.5
85
                                                                                                                                                                                                                                                                          83.5
                                                                                                                                                                                                                                                                                                                                                               82.5
82.5
82
                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
       엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19, Appl
21, Appl
22, Appl
22, Appl
37, Appl
35, Appl
181279,
3, Appl
14107, A
                                                                                                                                                    November 17, 2004, 15:22:38; Search time 81.3333 Seconds (without alignments) 631.334 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEPRYYESWT......VTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUDLISHED APPLICATIONS AND TO THE COMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US07_PUBCCMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB. DED: *

(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB. DED: *

(cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB. DED: *

(cgn2_6/ptodata/2/pu
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-293-239-17
US-10-177-390-30
US-10-293-239-19
US-10-293-239-21
US-10-293-239-28
US-10-293-239-28
US-10-293-239-22
US-10-293-239-35
US-10-293-239-35
US-10-437-965-181279
US-10-156-761-14107
US-10-156-761-13447
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                            1570615 segs, 354127592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                   US-10-705-716A-4
778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778
750.5
769.5
309
209
209
140
140
92.5
92.5
```

ö

Gaps

; 0

120

Result No.

```
Sequence 20, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TTILE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REPRENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOSTWARE: Patentin version 3.1
                                                                                                                          US-10-293-239-21

Sequence 21, Application US/10293239

Fublication No. US2030119043A1

GENERAL INFORMATION:

APPLICANT: Tanner. Stephan

TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia

TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia

TITLE OF INVENTION UNMBER: US/10/293,239

CURRENT FILING DATE: 2002-11-12

PRIOR FILING DATE: 2002-11-12

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLDSNGVPRSTAPGGIPNPEKKTNCET 120
121 QCPNPQSLSSGPLTQKQNGLQTTBAKRDAKRNPAKBVTINVTDSIQQMDRSRRITKNCVN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLBAEKS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLED 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.7%; Score 309; DB 14; Length 73; 96.6%; Pred. No. 5.5e-22; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.2%; Score 569.5; DB 14; Length 75.7%; Pred. No. 1.4e-46; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCPNPOSLSSGPLTOKONGLOTTE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 OCPNPOSLSSGPLTOKONGLOTTE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.7<sup>3</sup>
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L Similarity
56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-293-239-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-293-239-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-293-239-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tanner, Stephan APPLICANT: Tanner, Stephan APPLICANT: Tanner, Stephan APPLICANT: de la Chapelle, Albert
APPLICANT: de la Chapelle, Albert
TILE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
SOFFWARE: Patentin version 3.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS 60
                                                                                               Sequence 30, Application US/10177390
Publication No. US20030143743A1
GENERAL INFORMATION
GENERAL INFORMATION: Carold
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Bucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 30 absentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

96.5%; Score 750.5; DB 14; Length 180;
Best Local Similarity 80.6%; Pred. No. 8e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 778; DB 14; Length 145; Best Local Similarity 100.0%; Pred. No. 1.4e-66; Matches 145; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-293-239-19
. Sequence 19, Application US/10293239
. Publication No. US20030119043A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-177-390-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-293-239-19
                                                     RESULT 2
US-10-177-390-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

ř

Gaps

;

ö

```
us-lu-43/-yb3-lb1L/y
Sequence 181279, Application US/10437963
Fublication No. US20040123343A1
Fublication No. US20040123343A1
GENERAL INPORMATION:
FAPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 181279
LENGTH: 307
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/10293239

Sequence 35, Application US/10293239

Publication No US20030119043A1

GENERAL INCOMMATION:

APPLICANT: Tanner, Stephan

TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia

FILE REFERENCE: 22727/04101

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: US 60/348,210

PRIOR APPLICATION NUMBER: US 60/348,210

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 35

LENGTH: 18
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                Query Match 18.0%; Score 140; DB 14; Length 25; Best Local Similarity 100.0%; Pred. No. 2.3e-06; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 99; DB 14; Length 18; llarity 100.0%; Pred. No. 0.013; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(307)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                            1 RADAIEPRYYESWTRETESTWLTYT 25
                                                                                                                                                                                                                                                                                           7 RADAIEPRYYESWIRETESTWLTYT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 DAIEPRYYESWTRETEST 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DAIEPRYYESWTRETEST 18
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-293-239-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-293-239-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-437-963-181279
                      SEQ ID NO 37
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/10293239
Publication No. US2003019043A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tanner: Stephan
APPLICANT: Tanner: Stephan
APPLICANT: Tanner: Stephan
APPLICANT: Tanner: Stephan
APPLICANT: Tanner: 22/27/404101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR PELING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SSOFTWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 80
                                                                                          APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FITLE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
FURBENT APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REPERENCE: 22727/04101
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.7%; Score 293; DB 14; Length 80; 100.0%; Pred. No. 2.1e-20; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.4%; Score 299; DB 14; 1
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 54; Conservative 0; Mismatches 0;
                Sequence 18, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.(
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-10-293-239-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-293-239-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-293-239-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
```

g à

ò

.. 0

ð

셤 à g ò ద

```
63 NGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTE-----AKRDAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AGAMPEESAGGATTEEPSVGATTEKP----SAGATTEDPSAGATTEESPADAVAQQSAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GSRADAIEPRYYESWTRETESTWLTYTDSDAPPS--AAAPDSGPEAGGLHSGMLEDGLPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TNDSAPESDGGEQPPAGPEAGTAETGTPASATGT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 ARÁGVGKQTIYRWWSSKAEVLLEAFTĎLSÁQAAEÁAARPGPEEGGQEGGQENGIPDTG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 SRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.7%; Score 91; DB 14; Length 670; Best Local Similarity 25.4%; Pred. No. 6.8; Matches 32; Conservative 14; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.6%; Score 90; DB 14; Length 219; Best Local Similarity 33.9%; Pred. No. 2.1; Matches 20; Conservative 8; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ISHIKAWA, JUNA
APPLICANT: BHIBA, TADANOSHI
APPLICANT: SHIRAM, TADANOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156, 761
CURRENT FILING DATE: 2002-05-39
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13447
LENGTH: 219
                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29;
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697;
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02;
NUMBER OF EGQ ID NOS: 15109
SEROTH: 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 13447, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: INFEDA, HARRO
APPLICANT: ISHTKAWA, JUN
APPLICANT: HORIKAWA, HROSHI
APPLICANT: HORIKAWA, HROSHI
                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptomyces avermitilis
US-10-156-761-14107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 26, Application US/09910600
; Publication No. US20030036631A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 CHRGEGMSPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 RMPAKE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AAPAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-156-761-13447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-910-600-26
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bayer AG
TITLE OF INVENTION: REGULATION OF HUMAN INOSITOL POLYPHOSPHATE 5-PHOSPHATASE
FILE REPRENEUR: LIO235Porelagin Countries
CURRENT APPLICATION NUMBER: US/10/415,147
CURRENT PILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/243,745
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-030
SPIOR FILING DATE: 2001-031
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                  : | | : | : | : | : | : 138 | : : 143 PRLT---TPTPTPTSSTPRISISSIRRLLTPPPRCLITSHARRPPLQTHDRRRPLQSM 199
                                                                                                                                                                                                                                                                                                                                             78 EKKTNCETQCPNPQSLSSGP-----LTQKQNGLQTTEAKRDA----KRMPAKEV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 NGVPRSTAPGGIPNPEK-----KINC----ETQCPNPQSLSSGPLTQKQNGLQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 N----QTVPPPLPKPPRSPSRSPSRSPNRSPCVPPAPEVALPRPVTQGAGPGKCPSPNLQ 390
                                                                                                                                                                                                                                 -- LPSNGVPRSTAPGGIPNP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 EPRYYESWTRETESTWLTYTDSDAPP-----SAAAPDSGPEAGGLHSGMLEDGLPS 62
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.9%; Score 92.5; DB 15; Length 1001; Best Local Similarity 25.8%; Pred. No. 8; Matches 32; Conservative 15; Mismatches 48; Indels 29; Gaps
                                                                                                                                                                        39;
                                                                                                            Query Match 11.9%; Score 92.5; DB 16; Length 307; Best Local Similarity 27.8%; Pred. No. 1.9; Matches 37; Conservative 18; Mismatches 39; Indels 39
                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78569C.1.pep
US-10-437-963-181279
                                                                                                                                                                                                                              33 SDAPPSAAAPDSGPEA-GGLHSGMLEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14107, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10415147
Publication No. US20040043399A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADANOSHI
APPLICANT: SARAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 TINVIDSIQQMDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: |: ||
200 TVTXPDT--RLDR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 TTEA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 TOES 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-10-156-761-14107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-415-147-3
FEATURE:
```

පු

ð 엄 ઠે 엄

ð

ö

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 84, Application US/10036542

Publication No. US2030083481A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
FILE REFERENCE: PA002P1

CURRENT APPLICATION NUMBER: US/10/036,542

CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: OF/14,972

PRIOR APPLICATION NUMBER: 60/144,972

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 EAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCETQ-----CPNPQSLSSGPLTQK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CGGSRADAI-----EPRYYESWTRETESTW-LIYIDSDAPPSA-----AAPDS---GP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 SDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRS-TAPGGIPNPEKKTNCETQCPNPQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 SSTSTSSSFPSSFPSSSSSSSSSSCYPLIPS--TPEEVSADDETPNPPQ--SAQIACSSPS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: L3cyto-Y641
CTHER INFORMATION: alone
US-09-910-600-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.2%; Score 87.5; DB 14; Length 369;
Best Local Similarity 25.9%; Pred. No. 7;
Matches 28; Conservative 19; Mismatches 48; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 SLSSGPL-----TQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.3%; Score 88; DB 10; Length 298; Best Local Similarity 27.5%; Pred. No. 4.8; Matches 33; Conservative 18; Mismatches 43; Indels
APPLICANT: Change, Malinda
APPLICANT: Chang, Han
APPLICANT: Chang, Han
APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REFERENCE: D0003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PARENTIN Ver. 2.0
SEQ ID NO 26
LENGTH: 298
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
APPLICATION SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-036-542-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-036-542-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
```

.

20551, A 17311, A 29050, A

11, Appl 4, Appli 7, Appli 25380, A 29857, A 26994, A 12, Appl

Sequence Seq

Sequence Sequence

Sequence:

Run on:

Searched:

Database

Result No.

```
Query Match
11.2%; Score 87.5; DB 2; Length 369;
Best Local Similarity 25.9%; Pred. No. 0.34;
Matches 28; Conservative 19; Mismatches 48; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                             US-08-73-870-4

Sequence 4, Application US/08773870

Patent No. 5912143

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 9174 Porter Drive
CITY: Palo Alto
US-09-583-610D-2
US-09-252-991A-20551
US-09-252-991A-17311
US-09-252-991A-29050
US-09-496-320-11
US-08-435-678-4
US-08-435-678-4
US-08-252-991A-25380
US-09-252-991A-25380
US-09-252-991A-26994
US-09-252-991A-26994
US-09-252-991A-26994
US-07-757-022B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER EADABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette CONFORMER: DOS SOFTWARE: FALING DATE: Herewith CLASSIFICATION NUMBER: US/08/773,870

FILING DATE: Herewith CLASSIFICATION: 435

PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: TELENGLY NUMBER: 36,749

REFERENCE/OOCKET NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
   1088
254
381
381
1873
109
6402
655
655
1038
11049
11149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
   ; LIBRARY: GenB;
; CLONE: 533511
US-08-773-870-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
   Sequence 4, Appli
Sequence 16753, A
Sequence 25785, A
Sequence 81, Appl
Sequence 71, Appl
Sequence 2, Appli
Sequence 40, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 44, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 176, App
Sequence 174, App
Sequence 4200, Ap
Sequence 21052, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28271, A
23026, A
4, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18684, A
Sequence 20171, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 278, App
Sequence 993, App
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Appli
Sequence 4, Appli
                                                                                                                November 17, 2004, 15:02:57; Search time 24.3333 Seconds (without alignments) 395.183 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                             US-10-705-716A-4
778
1 MGCGGSRADAIEPRYYESWT.......VTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2
Sequence 4
Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ogn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-773-870-4
US-09-252-991A-25785
US-09-086-663A-81
US-09-086-663A-1
US-09-086-663A-71
US-09-086-663A-71
US-09-086-663A-71
US-09-086-663A-2
US-09-086-663A-2
US-09-086-663A-2
US-09-262-991A-21479
US-09-252-991A-21479
US-09-252-991A-28271
US-09-252-991A-28271
US-09-278-796A-23026
US-09-289-796A-23026
US-09-131-25-4
US-09-131-907A-2
US-09-131-907A-2
US-09-131-907A-2
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-252-991A-21052
US-09-252-991A-21052
US-09-1919-0393-278
US-09-1919-0393-278
US-09-1919-039-293
                                                                                                                                                                                                                                                                                                                            lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 using sw model
                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         687
2016
2016
2016
2016
305
305
160
217
441
707
                                                                                 OM protein - protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.5
78.5
78.5
78.7
78.7
78.7
77.5
77.5
                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
```

4

Gaps

13;

```
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 KSFTLTITVFTNPPQVATYHRAIKVTVDGPREPRRHRQKLDDSKPSLFSDRLSDLGRIPH 254
                                                                                                                                                                                         88 GTTGPTPPPAPTGKSSAAGGCAMPDCRHACRRRTARPPIPPVAPWISSTSRASVPGACTC 147
28 CGGSASIRPARAARPSPKPASSPTTAMTGSTRMTRPSPTSAKARPTPTTCGASASPATTP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----APDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DUCY, PATRICIA
APPLICANT: DUCY, PATRICIA
APPLICANT: KARSENTY, GERARD
TITLE OF INVENTION: OSF2/GBFA1 COMPOSITIONS AND METHODS OF USE
TILLE OF INVENTION: OSF2/GBFA1 COMPOSITIONS AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/086,663A
CURRENT FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/080,189
PRIOR PILING DATE: 1998-03-24
PRIOR APPLICATION NUMBER: 60/048,430
PRIOR APPLICATION NUMBER: 60/048,430
PRIOR PILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INPORMATION:
APPLICANT: DUCY, PARRICIA
APPLICANT: ARSENTY, GERARD
TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS OF USE
TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/086,663A
CURRENT FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/048,430
PRIOR APPLICATION NUMBER: 60/048,430
PRIOR PILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN VOICE: 2.1
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 80; DB 4; Length 528; larity 29.4%; Pred. No. 3.6; Conservative 7; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 PEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 PSMRVGVPPQNPRP-SLNSAPSPFNPQGQSQITDPRQAQSSP 295
                                                                                                                                                                                                                                                                                             90 POSLSSGPLTQKQNGLQTTEAKRDAK---RMPAKEVTINVT 127
                                                                                                                                                                                                                                                                                                                                                    148 PISSRIGPISRRRITIRCIAPIRCSRRYARRPAKKAITRCI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80; DB 4
Pred. No. 3.6;
7; Mismatches
                                                                                               GL-----PSNGVPRSTAPGGIPNPEKKTNCETQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-086-663A-81
; Sequence 81, Application US/09086663A
; Patent No. 6518063
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 82, Application US/09086663A; Patent No. 6518063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ESTWLTYTDSDAPPSAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
1 Similarity 29.4%;
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-086-663A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-086-663A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-086-663A-82
                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                          à
                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL APPLICATION NUMBER:
GENERAL FILING DATE:
1998-02-13
PRIOR APPLICATION NUMBER:
GENERAL INFORMATION INFORMATION:
GENERAL INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MAIC J. Rubenfield et al.

APPLICANT: MAIC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 NETPOSTDIPAAAVAKSNPKTNAEPAKIPNEKLLKTESPLSQKQNGATTTKEKSDVLLET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 NGVPRS--TAPGGIPNPEKKTNCE-TQCPNPQSL-SSGPLTQKQNGLQTTEAKRDA--KR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGSR----ADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLED 58
                                             SDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRS-TAPGGIPNPEKKTNCETQCPNPQ 91
                                                                                                         36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                            SECTION STREET SECTION SECTION
                                                                                                                                                                                                                                           SLSSGPL------TQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 85.5; DB 4; Length 316; 31.5%; Pred. No. 0.45; tive 12; Mismatches 38; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 MPAKEVTINVTDSIQQMDR-----SRRITK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 KSTSSTÍVSNANŠVLÓYTELSEIPIGVERÍTK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.4%; Score 81; DB 4;
Best Local Similarity 23.0%; Pred. No. 0.77;
Matches 37; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16753, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25'85, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 31.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-248-796A-16753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-248-796A-16753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-25785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 16753
LENGTH: 316
                                                                                                                                                                                                                                      92
                                             33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                       임
                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                             ð
```

ų,

```
Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-21479
                                                                                                                                                                                                                                                                                                                           US-09-086-663A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                           202 KSFTLITITVFTNPPQVATYHRAIKVTVDGPREPRRHRQKLDDSKPSLFSDRLSDLGRLPH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
  24 ESTWLIYIDSDAPPSAA-----APDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ESTWLTYTDSDAPPSAA-----APDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                  Sequence 71, Application US/09086663A
; Sequence 71, Application US/09086663A
; Patent No. 6518063
; GENERAL INFORMATION:
APPLICANT: DUCY, PATRICIA
; APPLICANT: KARSENTY, GERRAD
; TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: UTSC:525
; CURRENT PILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/080,189
; PRIOR FILING DATE: 1998-03-24
; PRIOR FILING DATE: 1998-03-24
; RICK RIGHS DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DUCY, PATRICIA
APPLICANT: DUCY, PATRICIA
APPLICANT: CARGENTY, GERRAD
TITLE OF INVERTION: OSF2/CHFA1 COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: UTSC:525
CURRENT PAPLICANTION NUMBER: US/09/086,663A
CURRENT PAPLICATION NUMBER: 60/080,189
PRIOR FILING DATE: 1998-03-24
PRIOR FILING DATE: 1998-03-24
PRIOR FILING DATE: 1998-03-29
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 80; DB 4; Length 548; 29.4%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 PSMRVGVPPQNPRP-SLNSAPSPFNPQGQSQITDPRQAQSSP 302
                                                                                                                        262 PSMRVGVPPQNPRP-SINSAPSPFNPQGOSQITDPRQAGSSP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 PEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                         77 PEKKTNCETOCPNPOSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09086663A
Patent No. 6518063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-086-663A-71
                                                                                                                                                                                                                             US-09-086-663A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-086-663A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                      g
```

US-09-086-663A-2

```
Sequence 21479, Application US/09252991A

Batent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                      ٠.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 ESTWLTYTDSDAPPSAA-----APDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPN 76
                                                                                                     24 ESTWLTYTDSDAPPSAA-----APDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ) OTHER INFORMATION: Peptide US-09-086-663A-80
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DUCY, PATRICIA
APPLICANT: DUCY, PATRICIA
APPLICANT: CARENTY, GERARD
TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: UTSC:525
CURRENT PELLING NUMBER: US/09/086,663A
CURRENT FILING DATE: 1998-05-29
PRIOR PILING DATE: 1998-05-29
PRIOR PILING DATE: 1998-05-29
PRIOR PILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 83
SOFTHARE: PATENTIN VET: 2.1
SEQ ID NO 80
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80; DB 4; Length 596;
Pred. No. 4.3;
7; Mismatches 57; Indels
     DB 4; Length 596;
Score 80; DB 4; Length 596
Pred. No. 4.3;
7; Mismatches 57; Indels
                                                                                                                                                                                                   77 PEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                                                                                                                                                                     77 PEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 PSMRVGVPPONPRP-SINSAPSPFNPOGOSQITDPROAQSSP 370
                                                                                                                                                                                                                                                                                                                                                                            Sequence 80, Application US/09086663A Patent No. 6518063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
     10.3%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                      30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.4
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 21479
LENGTH: 330
```

```
---AGSASRSTAPGSWPGPRAAGSGRAWPRPCPTLPRCSS 210
                                                                                                                                                                                                           40 -AAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPEKKTN-----CET--QCPN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                     52;
                                                                                                                                        --ETESTWL----TYTDSDAPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: RAZ, AVRAHAM
TITLE OF INVENTION: A METASTASIS IN A CELL SAMPLE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Dykema Gossett
STREET: STE SOS N. Woodward
CITY: Bloomfield Hills
                                                               Score 78; DB 3; Length 230;
Pred. No. 1.9;
9; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.0%; Score 78; DB 1; Length 264; 33.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08562311
Patent No. 5801002
                                                                 10.0%;
26.7%;
                                                                                                                                                                                                                                           162 PSRPGSSPTRSW-----
                                                                                                                                                                                                                                                                                90 PQS---LSSGPLTQK 101
                                                                                                                                                                                                                                                                                                                211 SSSSSRASSGPSDRK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810-540-0849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 264 amino acids
amino acid
                                                               Query Match
Best Local Similarity 26.7'
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 810-540-0763
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Conservative
                                                                                                                                        8 ADAIEPRYYESWTR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.
                  ORGANISM: maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                US-09-248-335-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     US-08-562-311-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-562-311-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                        d
                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                     Sequent No. 6673549

Batent No. 6673549

GRNERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION WUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
                                                                                                                                                                                                298 YRRWSAEVISS--TYSDEDRPPK--VPPREPLS------PSNS--RTPSPKSLP 339
                                                                                                                             16 YESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIP 75
                                                                                                   2 GCGGSRADAIE------39
                                                                                                                                                                        40 -AAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPEKKTW--CETQCPNPQSLSSG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Indels 27; Gaps
                                                                      Gaps
                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/09248335
Sequence 46, Application US/09248335
Sequence 47, Application US/09248335
Sequence 47, Application US/09248335
SETILE NFORMATION:
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTAN: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
TITLE OF INVENTED APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 44
LENGTH: 230
                             10.1%; Score 78.5; DB 4; Length 330; 26.2%; Pred. No. 2.7; tive 13; Mismatches 50; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.1%; Score 78.5; DB 4; Length 462;
Best Local Similarity 28.6%; Pred. No. 4.4;
Matches 30; Conservative 16; Mismatches 32; Indels 2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 NPEKKTNCETQ -- CPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 SYLNGVMPPTQSFAPDPKYVSSKAL-QRQN-----SEGSASKVP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2716815CD1
US-09-976-594-427
              Query Match
Best Local Similarity 26.2.
Thes 34; Conservative
                                                                                                                                                                                                                                           97 PLTQKQNGLQ 106
                                                                                                                                                                                                                                                                              138 PARRODPGLÓ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-09-252-991A-21479
                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-976-594-427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-248-335-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 427
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                    g
                                                                                                                                                                        ò
                                                                                                                                                                                                         g
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

48;

```
60 LPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLT--QKQNGLQTTEAKRDAKRM 117
                                                                                                                                                                                                                                                                                                     482 TETTESTKTTETTKTTGPAETTDLAESTDDLNESSAPPPTEDPSDIPSATTTDEATVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 687;
                                                                                                                                   11; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 PAKEVIINVIDSIQOMD-----RSRRITKNC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 -TTETTATVTDCEDGDDSCTPRTTIRSTVITTHC 617
                          cn
1 Similarity 26.6%; Pred. No. 8.7;
41; Congervative 11; Mismatchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 17, 2004, 15:30:03 Job time: 25.3333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09634920 Patent No. 6342357 GENERAL INFORMATION:
                                                                                                                                                                                                                      20 TRETESTWLTYT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-634-920-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-634-920-4
                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
RIOR APPLICATION NUMBER: US 60/096,409
REAL OF SEQ ID NOS: 28208
SEQ ID NO 23026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: UNSURE; LOCATION: (388), (687); OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno US-09-248-796A-23026
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2821, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR SEQ ID NOS: 33142
SEQ ID NO 28271
LENGTH: 312
                                                             60 LPSNGVPRSTAPGGIPNPEKKTNCE------TQCPNPQSLSSGPLTQKQNGLQT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 EPPYPAQGARRIGA-----RRPRAAAPGQGHPGPGGADDLPDGRRQRLHRVALGPG 89
35 APPSA---AAPDS---GPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCETQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 EPRYYESWTRETESTWLTYTDSDAPPSAAAPDSG-PEAGG-----LHSGMLEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 78; DB 4; Length 312; 26.3%; Pred. No. 2.9; tive 10; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23026, Application US/09248796A
Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginos
                                                                                                                                                                                                                          | ::||||
113 GGYPAAGPYGVPAGPLT 129
                                                                                                                                                                          -----NPQSLSSGPLT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 TEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.09
Best Local Similarity 26.39
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-248-796A-23026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-28271
                                                                              g
                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
```

```
SERBEMAL INFLANTIAL SUBJEMSKI, IGOR
APPLICANT: Splawski, Igor
APPLICANT: Splawski, Igor
TITLE OF INVENTION: ALTERATIONS IN THE LONG OT SYNDROME GENES KVLQT1 AND
TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME
TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME
FILE REPERENCE: 2323-155
CURRENT APPLICATION NUMBER: US/09/634,920
CURRENT FILING DATE: 2000-03-09
FRIOR PRILING DATE: 2000-03-17
FRIOR PRILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LEAST OF THE STORM OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 EDGLPSNGV-----PRSTAPGG----IPNPEKKINCETQCPNPQSLSS-GPLTQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 GSRADAIEPRYYESWIRETES-----TW-LIYIDSDAPPSAAAPDSGPEAGGLHSGML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.0%; Score 78; DB 3; Length 2016; Best Local Similarity 25.5%; Pred. No. 39; Matches 42; Conservative 23; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 KONGLOTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 145
```

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 17, 2004, 15:00:21; Search time 19.6667 Seconds (without alignments) 709.395 Million cell updates/sec

US-10-705-716A-4 778 Title: Perfect score:

1 MGCGGSRADAIEPRYYESWT.......VTDSIQQMDRSRRITKNCVN 145 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\* Database :

piri: \* piri: \* piri: \* piri: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	prot	igen	unknown protein, 4	microtubule-associ	E2 protein - deer	probable ppp prote	colc	crtA protein - Rho	neural cell adhesi	probable large Pro	integrase-like pro	hypothetical prote				hypothetical prote		sarcalumenin precu	SEC14 protein homo	bifocal protein -	protein-tyrosine-p	hypothetical prote	atrophin-1 related	υ	nascent polypeptid	probable periplasm	Ω	probable transmemb
SUMMARIES		T47424	H86464	138659	A96717	A45301	WZWLDP	H70699	140333	S49619	IJMSNI	T35985	S22571	B90784	D85644	A85359	T50744	T23728	A48233	A33280	T41244	T03743	T14355	AC2512	T42731	S71461	T30826	F82029	598	T35659
	DB	2	N	~	~	~	Н	7	N	N	-4	N	~	~	N	C)	N	7	7	~	7	~	7	7	~	7	N	7	7	7
	Length	1122	069	369	860	733	416	514	672	327	1115	1366	499	2793	2806	263	327	476	513	806	1008	1063	1494	444	1006	2157	2187	197	264	396
ak	Query Match	11.5	11.4	11.2	11.2	10.9	10.8	10.8	10.8	10.7	10.7	10.6	10.5	10.5	10.5	10.3	10.3	10.3	10.3	10.3	10.2	•		10.2					10.0	10.0
	Score	89.5	88.5	87.5	87.5	84.5	84	84	84	83.5	83.5	82.5	81.5	81.5	81.5	80.5	80.5	80	80	80	79.5	79.5	79.5	79	79	79	79	78	78	78
	Result No.		7	e	4	ស	9	7	00	σ	10	11		13		15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

BDLF2 protein - hu	protein F40H6.5 [i	sodium channel pro	spliceosome-associ	hypothetical prote	aggrecan precursor	unconventional myo	attachment protein	mucin 7 precursor,	PTB-associated spl	SERA antigen/papai	hypothetical prote	neural cell adhesi	fibroin-3 related
QQBE44 JC4155	F88473	A38195	A47655	T00039	I50421	A59295	JQ1205	A48018	A46302	H71616	C83632	A60058	T49510
	0	9	1 (1	7	-	~	N	~	N	7	7	7	7
420	1216	2016	464	906	2109	3511	297	377	707	1100	264	421	670
10.0	10.0	10.0	10.01	10.0	10.0	10.0	9.9	9.9	6.6	6.6	9.6	9.6	9.8
78	78	78	77.5	77.5	77.5	77.5	77	77	77	77	76.5	76.5	76.5
30	32	33	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

T47424
hypothetical protein T22K7.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 09-Jul-2004
C;Accession: T47424
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24459
A; Accession: T47424
A;Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1122 <rie></rie>
A;Cross-references: UNIPROT:Q9M291; EMBL:AL138641
A; Experimental source: cultivar Columbia; BAC clone T22K7
C,Genetics:
A.Man nogition: 3

A;Map position: 3 A;Introns: 303/3; 363/3; 388/3; 421/3; 459/1; 501/3; 552/3; 579/3; 605/3; 636/3; 655/1; 6 A;Note: T22K7.20

Gaps ch 11.5%; Score 89.5; DB 2; Length 1122; Similarity 28.4%; Pred. No. 10; 23; Conservative 10; Mismatches 31; Indels 17; Query Match Best Local Similarity Matches 23; Conserva

3;

36 PPSAAAP----DSGPEAGGLHSGMLEDGLPSNGVPRS-----TAPGGIPNPEKKT 81 q ò

242 SGPMMAPPPYGQPPNAGPFT 262 82 NCETQCPNP---QSLSSGPLT 99 ઠે

RESULT 2

H86464

Prypothetical protein F12G12.9 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: H86464
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alaute 408, 816-820, 2000
A; Authors: Hunter, J.L.; Dewins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 10f the plant Arabidopsis.
A; Freference number: A86141; MUID:21016719; PMID:11130712

A;Accession: H86464 A;Status: preliminary

```
A;Title: "w, w.; ru, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Recession: A96717
A;Retus preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S31658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GSRADAIE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-860 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 TQ 100
                                                                                                                                                                                                                                                                                                                                                                                    A; Genetics:
A; Gene: F23010.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanoma antigen MAGE-10 - human
C;Species: Homo sapiens (man)
C;Daces: O'Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 138659
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Redidues: 1-569 <RES>
A.Cross_references: UNIPROT: P43363; EMBL:U10685; NID:9533510; PIDN:AAA68869.1; PID:95335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chaccesion: A96717

RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fam
                                                                                                          A;Residues: 1-690 <STO>
A;Croser references: UNIPROT:Q9FX17; GB:AE005172; NID:g10086468; PIDN:AAG12528.1; GSPDB:
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE A,Reference number: 138659; MUID:95012457; PMID:7927540
A,Accession: 138659
                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPGTPTATQASSTSSEKSKTPTSIPSTPTTPQRSSTESTETPMSSPVITQPSPSASSIP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 YDSNTEKVSTT--LFTPDDFPPLPVSSRAVVIPESGEQSSECTTGFDPASIGNNS---TS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 YESWTRETESTWLTYTDSDAPP----SAAAPDSGPEAGGLHSGMLEDGLPSNGVPRST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRS-TAPGGIPNPEKKTNCETQCPNPQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown protein, 45065-49536 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar.2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              62; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: | | | :: | | : | :| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLSSGPL-----TQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQ 131
                                                                                                                                                                                                                                                                                                                 Query Match 11.4%; Score 88.5; DB 2; Length 690; Best Local Similarity 20.5%; Pred. No. 7.2; Matches 33; Conservative 29; Mismatches 62; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 APGGIPNPEKKTNCETQ-CPNPQSLSSGPLTQKQNGLQTTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AKRDAKRMPAKEVTIN--VTDSIQQMDRSRRITKNCV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 TMHAATSSASTSQQSSVASNKSTTDVVQIQEASPKSTAPCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.2%; Score 87.5; DE 25.9%; Pred. No. 4.2; tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Superfamily: tumor associated protein MAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenetics 40, 360-369, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.9%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: GDB:WAGEA10; WAGE10
A,Cross-references: GDB:331126
A,Map position: Xq28-Xq28
A,Introns: #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
A,Cross-references: UNIPROT:Q9C982; GB:AE005173; NID:g7705093; PIDN:AAF67772.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microtubule-associated protein tau - mouse
N;Alternate names: microtubule binding protein tau
C;Species: Mus musculus (house mouse)
C;Accession: A45301, 531658
R;Couchie, D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 4378-4381, 1992
A;Title: Primary structure of high molecular weight tau present in the peripheral nervox
A;Reference number: A45301; MUID:92262443; PMID:1374898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A45301
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-733 <COUS
A;Cross-references: UNIPROT:P10637
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: extracted from NCB1 backbone (NCBIN:102045, NCBIP:102046)
B;Kenner, L.; Forstner, M.; Hutter, H.; Hoefler, G.; Kurzbauer, R.; Zatloukal, K.; Kriss submitted to the EMBL Data Library, May 1992
A;Description: First observation of mRNA for a tau-protein from murine liver and kidney
                                                                                                                                                                                                                                             .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 GRAAPQAG---SGSVCGETAS--VPGLPTEGSVPLPADFFSKVSAETQASQPEGPGTGPM 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                             TESTWLTYTDSDAPPSAAAPDSG-PEAGGLHSGMLEDGLPSNGVPRSTAP-GGIPN---P 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---PRYYESWTRE-----TESTWLTYTDSDAPPSAAPDS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Accession: S31658
A/Status: preliminary
A/Molecule type: mRNA
A/Rocession: S31658
A/Status: preliminary
A/Molecule type: mRNA
A/Rocession: S21658
A/Cross-references: EMBL:Z12133; NID:g54263; PIDN:CAA78121.1; PID:g388534
C/Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C/Keywords: microtubule binding; tandem repeat
F/544-574/Domain: MAP2/tau repeat homology <MT1>
F/575-605/Domain: MAP2/tau repeat homology <MT2>
F/566-636/Domain: MAP2/tau repeat homology <MT2>
F/566-636/Domain: MAP2/tau repeat homology <MT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G---PEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPE---KKTNCETQCPNPQSLSSGPL
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 84.5; DB 2; Length 733; 26.2%; Pred. No. 17; ive 16; Mismatches 43; Indels 31
                                                                                                                                                                          Length 860;
                                                                                                                                                                                                                                      36; Indels
                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                78 EKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 NTGTN--TGMPN----SNGMPTSSS 176
                                                                                                                                                                   ; Score 87.5; DB
; Pred. No. 11;
9; Mismatches
                                                                                                                                                                      ch 11.2%;
1 Similarity 31.2%;
29; Conservative
```

```
NAILCRAIN CONTINUES.

(Species: Bordetella pertussis

(Species: Species: Spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          States Share-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Species: Shar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49619
R;Lang, H.P.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N.
submitted to the EMBL Data Library, November 1994
A;Description: The complete DNA sequence, specific TNS insertion map and gene assignment
A;Reference number: S49619
A;Status: preliminary
A;Recession: S49619
A;Status: preliminary
A;Residues: 1-327 <LAN>
A;Residues: 1-327 <LAN>
A;Residues: 1-327 <LAN>
A;Genetics:
A;Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q45343; EMBL:U16754; NID:g984282; PIDN:AAC43453.1; PID:g9842
A;Experimental source: strain 18323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 وُ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 HKDNPSPPVVGVGPGMAESSGGHNPGVGGGTHENGLPGIGKVGGSAPGPGGLGRNDENSE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 YIDSDAPP----SAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTA--PGGI----PNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 DSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNP-EKKTNCETQCPN----PQSLSSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 SSLNPGTLGPSPGPDTSTGSGPDAGMASGAGSTSPGASGGAGKDA--MPPSE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 KKTNCETQCPNP---QSLSSGPLTQKQNGLQTTE-----AKRDAKRMPAKE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: tcfA
F;l-39/Domain: signal sequence #status predicted <SIG>
F;40-672/Product: tracheal colonization factor A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 327;
                                                                                        tracheal colonization factor A precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 672,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GCGGSRADAIEPRYYESWTRE------TESTW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.8%; Score 84; DB 2
Best Local Similarity 31.2%; Pred. No. 17;
Matches 35; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.7%; Score 83.5; D 23.9%; Pred. No. 8; Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 LTOKONGLOTTEAKRDAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 KPFRSRGLEADAAGREAE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.99
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        849619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P71588; GB:Z80233; GB:AL123456; NID:g3261645; PIDN:CAB02438.
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 SGMLEDG------LPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                        E2 protein - deer papillomavirus
C;Species: deer papillomavirus
A;Note: host Odocoileus virginianus (American white-tailed deer)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Feb-1994
C;Accession: A03673
R;Groff, D.E.; Lancaster, W.D.
A;Virol. 56, 85-91, 1985
A;Title: Molecular cloning and nucleotide sequence of deer papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAP-----PSAAAPDSGPEAGGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GGSRADAI-----EPRYYESWTRE----TESTWLTYTDSDAP-PSAAAPDSGPEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 GGLHSGMLEDGLPSNGVPRS---TAPGG-----IPNPEKKTNCETQCPNPQSLSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: ppp
F;35-243/Domain: conserved hypothetical protein yloO homology <YLOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ppp protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 84; DB 1; Length 416;
Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 10.8%; Score 84; DB 2; Similarity 25.9%; Pred. No. 12; 36; Conservative 10; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 84; 22.31.7%; Pred. No. 9.6; tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 1-416 <GRO>
C, Superfamily: papillomavirus E2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 KONGLOTTEAKRDAKRMPA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SPITSAPAPIGITPA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.7%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: papilicumari
C; Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-514 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A03673
凹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

d à qq

ð

neural cell adhesion molecule 1 precursor, long domain splice form - mouse

ð 셤 à g ઠે 4

9

881

65

```
EMBL: AL035559; PIDN: CAB37473.1; GSPDB: GN00070; SCOEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             integrase-like protein FE65 - rat
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: 822571; 822572
R;Duilio, A.; Zambrano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, T.
R;Duilio, A.; Zambrano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, T.
A;Title: A rat brain mRNA encoding a transcriptional activator homologous to the DNA bir A;Reference number: 822571; MuID:92020215; PMID:1923810
A;Accession: 822571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;MOlecule type: mRNA
A;Residues: 1-499 <DUII>
A;Crose-references: UNIPROT:Q99MK3; EMBL:X60469; NID:g57559; PIDN:CAA42999.1; PID:g5756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                 66 -PRSTAPGGIPNPE---KKTNCETQCPNPQSLSS------GPLTQKQNGLQTTEAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 GAGAARR-----PTWAKEAPS------PPASTAPEPWSGPGGAVGEAGGVSSP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable large Pro/Ala/Gly-rich protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Accession: T35885

R; Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajand submitted to the EMBL Data Library, February 1999

A; Reference number: Z21589

A; Recession: T35885

A; Rocession: T35885

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Roceule : L1566 c/MIR>
A; Residues: 1-1366 c/MIR>
A; Residues: 1-1366 c/MIR>
A; Resperimental source: strain A3(2)
                                                                                                                                                                                                      830 TNSDITTETFATAQNSPISET-TILISSIAPPATTVPDSNSVPAG------QATPSKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Mosidues: 31-318 cDU12>
A;Cross-references: EMBL:X60468; NID:957561; PIDN:CAA42998.1; PID:gll77617
A;Note: this sequence was submitted to the EMBL Data Library, July 1991
                                                                                                     6 SRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGV
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Gaps
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 GTGLRGSGTVAAGGVPLFGARGGVSGAAGGVPLPTVFTASEPR-PGP 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 88/3; 107/3; 135/3; 157/3; 250/2; 252/2; 290/3
C;Keywords: transcription regulation
F;42-78/Domain: WW repeat homology <WW1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Indels
     59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GMLEDG-LPSNGVPR----STAPGGIPNPEKKTNCETQCPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGGSRADAIBPRYYESWTRETESTWLTYTDSDAPPSAAAPD--SGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.6%; Score 82.5; D
Best Local Similarity 30.8%; Pred. No. 51;
Matches 33; Conservative 12; Mismatches
     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 PASKASPAPTPT 952
     35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDAKRMPAKEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SCOEDB:SC9F2.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S22572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                           ð
                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
NyAlternate names: NCAM-180
NyContains: neural cell adhesion molecule, short domain splice form (NCAM-140)
NyContains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C;Species 31-Mar-1993 Hesquence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A29673; S00844; $00384; A28281; A44290; S00383
C;Accession: A29673; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fonted BMD J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A;Reference number: A29673; MUID:87246524; PMID:3595563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: A29673
A,Accession: A29673
A,Molecule type: mRNA
A,FResidues: 1-548, T'.550-571, T'.573-574, D'.576-588, MQPS',593, S'.595-599, P'.601, L'
A,Cross-references: UNIPROT:P13595; EMBL:Y00051; NID:953342; PIDN:CAA68263.1; PID:953343
A,Cross-references: UNIPROT:P13595; EMBL:Y00051; NID:953342; PIDN:CAA68263.1; PID:953343
B,Santoni, M.J.; Barthals, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W
Nucleic Acids Res. 15, 8621-8641, 1987
A,Feference number: S00844; MUID:88067687; PMID:3684567
A,Accession: S00844
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
A; Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C; Superfamily: neural cell adhesion; cell adhesion; duplication; heparin binding; si F;1-19/Domain: signal sequence #status predicted <SIGs
F;20-1115/Froduct: neural cell adhesion molecule, long domain splice form #status experi F;20-711/Domain: extracellular #status predicted <EXTS
F;20-711/Domain: extracellular #status predicted <EXTS
F;34-98/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;132-191/Domain: immunoglobulin homology <IRM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;226-270/Domain: immunoglobulin homology <IRM3>
F;262-272/Region: NCAW binding #status predicted
F;233-388/Domain: immunoglobulin homology <IRM3>
F;2420-482/Domain: immunoglobulin homology <IRM4>
F;240-685/Domain: fibronectin type III repeat homology <FN3B>
F;519-759/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: intransmembrane #status predicted <IRM3>
F;712-729/Domain: intransmembrane #status predicted <IRM3>
F;713-1115/Domain: intracellular #status predicted <IRM3>
F;710-7115/Domain: intracellular #status predicted <IRM3-7115/Domain: i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: protein.
;Residues: 20-36 <ROU>
;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol;
;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Barthels, D.; Vopper, G.; Wille, W.
Nuclaic Acids Ree. 16, 4217-4225, 1984
A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A;Reference number: A28281; MUID:88247737; PMID:2454455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 529-809,1077-1115 <SAN>
A; Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; PID:g817984
A; Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; PID:g817984
B; Barbas J. A.; Chaix, J. J.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-622, 1988
A; Title: Differential splicing and alternative polyadenylation generates distinct NCAM
A; Reference number: S00382; MUID:88283628; PMID:3396534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 804-1081 - 6EB3>
A; Cross-references: EMBL: 207244; NID: 953321; PIDN: CAA30230.1; PID: 9929720
B; Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A; Title: Structural and immunological characterization of the amino-terminal domain of
A; Reference number: A44290; MUID: 86140120; PMID: 3512556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 642-1115 <BAR>
Cross-references: EMBL:X07195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S00384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A44290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A28281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Map position: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: NCAM
```

8;

DB 2; Length 499;

Score 81.5; I Pred. No. 19;

10.5%;

Best Local Similarity

Query Match

DB 1; Length 1115;

Score 83.5; I Pred. No. 33;

10.7%; 26.5%;

Query Match Best Local Similarity

Conservative

40;

Matches

ð d Db

8 셤

à

```
translation initiation factor-like protein [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;bacession: Asabidopsis thaliana (mouse-ear cress)
C;bacession: A85359
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUD:20083488; PMID:10617198
A;Accession: A85359
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPROT: Q9SUHB; GB:NC_001268; NID: 97269969; PIDN: CAB79786.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 --LPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRM 117
           | | : | | : | | : | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ALVQGNG---SQQPKPVPSPTRQT-VEKPKPQPQPQBVAPPT--TTSLNTVELSRKTNSL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 GRGGSRRFA--PRF-----TLSSSSDLTNGGDAPSFAVKGSG------GLLNDRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                              93 LSSGPLTQKQNGLQTTEAKRDA---KRMPAKEVTINVTDSIQQMDRSRRI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.3%; Score 80.5; DB 2; Length 263; Best Local Similarity 28.1%; Pred. No. 11; Matches 38; Conservative 13; Mismatches 57; Indels 2
                                                                                                                                                                                                                                                                Search completed: November 17, 2004, 15:28:53
Job time : 21.6667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | |
112 LEEYFNVRLLDEALO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 PAKEVTINVTDSIQQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-263 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: AT4930680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein ECs1242 [imported] - Escherichia coli (strain O157:H7, substrain RI C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Bs.Uul-2001 #sequence_revision 18-Uul-2001 #text_change 09-Uul-2004 C;Accession: B90784 [S;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q8X2Q2; GB:BA000007; PIDN:BAB34665.1; PID:g13360702; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                 9
                                                                                                                                                                                                                                                                                                                                                                                                            51 LHSGMLEDGLPSNGVPRSTAPG--GIPNPEKKTNCETQCP-NPQSLSSGPLTQKQNGLQT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791 APENAA----GROGETLEGDMVRRGLPSPDAQNATAPVREGLPAPDIARN--VRMPQPES 844
                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                             94
                                                                                                              13 PRYYES-----WTR--ETESTWL----TYTDSDAPPSAAAPDSG--PE----AGG
                                                                                                                                                                                                                       35 PNAFETDSDLPAGWMRVQDISGIYYWHIPIGITQWEPPGRASPSOGNSPQEESQLTWTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 APPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAP--GGIPNPEKKTNCETQCPNPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels 11; Gaps
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 LSSGPLTQKQNGLQTTEAKRDA---KRMPAKEVTINVTDSIQQMDRSRRI 139
                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 81.5; DB 2; Length 2793; 27.3%; Pred. No. 1.4e+02; Live 15; Mismatches 54; Indels 11.
     67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 TEAKRDAKRMPAKEV-TINVTDSIQOMDRSRRITKNCV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 RNANPGIKCFAVRSLGWVEMTEEELAPGRSSVAVNNCI 187
20; Mismatches
```

A,Residues: 1-2806 <STO> A,Cross-references: UNIPROT:Q8X470, GB:AE005174; NID:g12514354; PIDN:AAG55616.1; GSPDB:G A,Experimental source: strain O157:H7, substrain EDL933

A;Accession: D85644 A;Status: preliminary A; Molecule type: DNA 4

54; Indels 11;

Length 2806;

Query Match
10.5%; Score 81.5; DB 2;
Best Local Similarity 27.3%; Pred. No. 1.4e+02;
Matches 30; Conservative 15; Mismatches 54;

35 APPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAP--GGIPNPEKKTNCETQCPNPQS 92

hypothetical protein 21495 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9 C.Species: Escherichia coli C.Date: 16-Feb\_2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

| : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :

30; Conservative

Local Similarity

Best Loc Matches

g

à q

à

A; Gene: ECs1242

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-2793 <HAY>

C,Accession: D85644
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

```
5198347-4
;Patent No. 5198347
                                                                                                                                                                                                                                                                                                                                                ;SEQ ID NO:4:
; LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-08-374-077C-2
5198347-4
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 176, App
Sequence 176, App
Sequence 177, App
Sequence 177, App
Sequence 178, App
Sequence 178, App
Sequence 173, App
Sequence 16753, App
Sequence 1753, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131, App
7679, Ap
2, Appli
6, Appli
2, Appli
2, Appli
21991, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2, Appli
59848, A
44417, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43579, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Appli
Sequence 21991, A
Sequence 43579, A
Sequence 42538, A
Sequence 2, Appli
                                                                   2004, 15:02:57; Search time 24.3333 Seconds (without alignments) 395.183 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18938,
                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                1 MGCGGSRADAIEPRYYESWT.......VTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                       /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-374-077C-2
US-08-374-077C-2
US-09-13-90-2
US-09-13-90-2
US-09-121-964-1
US-09-121-964-1
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-071-035-174
US-09-328-352-8115
US-09-338-352-8115
US-09-338-092-131
US-09-338-092-131
US-09-254-325-2
US-09-254-325-2
US-09-254-325-2
US-09-254-325-2
US-09-274-325-2
US-09-274-325-3
US-09-274-357-3
US-09-270-767-43579
US-09-371-461-2
US-09-371-461-2
US-09-371-461-2
US-09-371-461-2
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-4358
US-09-270-767-59848
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                Issued Patents AA:*
                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                            US-10-705-716A-8
767
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   November 17,
                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5
                                                                                                            Title:
Perfect score:
                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.5
80.5
80.5
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.5
75.5
74
73.5
73.5
                                                  OM protein
                                                                                                                                  Sequence:
                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                Database
                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

```
17765, A
30546, A
26962, A
26963, A
9, Appli
3, Appli
7467, Ap
19245, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41874, A
19505, A
1, Appli
17, Appl
10, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGV-LRPAAPGGIANPEKKMNC-GTQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                    Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08374077C; Patent No. 6027912; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
APPLICANT: Ren, Delian
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
TITLE OF INVENTION: Calcium Channel Subunit
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READBLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPPLICANT: Miller, LOUIS H.; ADAMS, JOHN H.; KASLOW, JDAVIC C.; FANG, XIANGDONG TIALE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND FLASMODIUM YOWLESI DUFFY RECEPTOR CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/554,837
FILING DATE: 20-JUL-1990
US-09-252-991A-17765
US-09-252-991A-30546
US-09-252-991A-27673
US-09-252-991A-27673
US-09-235-153-3
US-09-235-153-3
US-09-252-991A-19245
US-09-252-991A-19245
US-09-270-767-41874
US-09-270-767-41874
US-09-270-767-41874
US-09-270-767-41874
US-09-270-767-41874
US-09-270-767-41874
US-09-33-271A-19505
US-09-33-271A-19505
US-08-158-232-10
US-08-158-232-10
US-08-316-301A-12
US-08-316-301A-12
US-08-316-301A-12
US-08-611-928-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.4%; Score 87.5; Dl
31.8%; Pred. No. 0.4;
tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 NSQNLSS-GPLTQKQNGLWATEAKRDAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDRSQGSLGPHTDERATLGETHMEKDTE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.8
Matches 28; Conservative
```

```
NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 022650-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/111,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/374,077
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09539879A
Patent No. 6436627
GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
Ren, Dejian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703-836-202
                                                                                                                                                                                                           10.5%;
               TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                               LENGTH: 2516 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2
703-836-6620
                                                                                                                                                                                                                Query Match 10.5%
Best Local Similarity 22.4%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-895-590-2
                                                                                                        amino acid
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-539-879A-2
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                              염
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 DDNSSY--SAVGGDSSSSNSCNCDITGDNSTLHGLGVGDVCSFIADCDDNSEDDDGDPNN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CGGSRADAIEPRY--YESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 QNLSSGPL-TQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08895590
Patent No. 6207410
GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 80.5; DB 3; Length 2516; 22.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59; Indels
             SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,077C FILING DATE: US/08/300 REFERENCE/DOCKET NUMBER: 022650-264 TELEPROMUNICATION INFORMATION: TELEPROMUNICATION: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WADUTER: IBM PC compatible
"WATEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    022650-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/374,888
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SSNGVLRPAAPGGIANPEKKOMC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 39,300 REFERENCE/DOCKET NUMBER: 02: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          : 2516 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McGowan, Malcolm M
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.4%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                            US-08-374-077C-2
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-895-590-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
ω
ω
                                                                                                                                                                                                                                          3 CGGSRADAIEPRY--YESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
                                                                                                                                                                                                       61 SSNGVLRPAAPGGIANPEKKMNC-------GTQC-------PNS 90
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                        308 QDLSSQTLRTAAIVAAVAAAKEQAQEQSLADCE-SFSDRRQDADEDVRIIQDC 360
                                                                                                                                                                                                                                                                                                             91 ONLSSGPL-TOKONGLWATEAKRDAKRMSAREVAINVTENIROMDRSKRVTKNC
                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zheng, Wei
Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
Calcium Channel Subunit
                                                                                                                                                    207 CGGGGISAPPRLTPEEAWQLQPQ-----NSVTSAGSTNSSFSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PLOPPy disk

COMPUTER: PLOPPy disk

COMPUTER: PLOPPY SERVING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/539,879A

FILING DATE: 31-Mar-2000

CLASSIFICATION: <Unknown>
                                                   23; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
Score 80.5; DB 3;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
```

ð g

셤

ò

g

```
GENERAL INCORNATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 32740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 176, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 -------RPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 AAARKSAVQLQGMHAGDAENGIHAVVGQQADQGLAGGEGLLWLHGQYPHPVRRPSESPFA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 PQRSCSHSHKREGEPSCPPGLQPLASRINAST-----ASAPSASASNGLTSSSSKRS 528
                                                                                                                                                                                                                                                     2 STTIEVTOKDLHDLLEIFEKKPFDAGSCEKGSLEEDITNRCEFLFKKDYTLIELDNSNGV 61
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                        66 LRPAAPGGIANPE-----KKWNCGTQCPNSQNLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                       LSPRYPGRIFIPBYEHGHMTSTITPNNTNLGTQATNHASPQSG---KNGNGL 110
                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 A-----KRMSAREVAINVTEN-----IRQMDRSKRVTKNCI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.7%; Pred. No. 4.6;
Matches 31; Conservative 8; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.0%; Score 77; DB 4; Length 715; Best Local Similarity 17.9%; Pred. No. 5.8; Matches 30; Conservative 25; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                        25 STWLTYTDSDALPSAAATDSGP-EAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32740, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 AAATDSGPEAGGLHAGVLEDGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
; TYPE: PRT
; ORGANISM: Sarcophaga peregrina
US-09-121-964-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-09-252-991A-32740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-32740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-09-071-035-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT:
MARC J. Rubenfield et al.
APPLICANT:
MARC J. Rubenfield et al.
APPLICANT:
MARC J. Rubenfield et al.
APPLICANT:
MARC J. RUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABCUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18465
LENGTH: 244
                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                ----GTQC------PNS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GIOCPNSON-- 92
                                                                                                                                                                           3 CGGSRADAIEPRY--YESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GCGGSRADAIEPRYYESWTRETESTWLT----YTDSDALPSAAATDSGPEAGGLHAGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 --LSSGPLTQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONLSSGPL-TOKONGLWATEAKRDAKRMSAREVAINVTENIROMDRSKRVTKNC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1. Application US/09121964

Patent No. 6124447

Sequence No. 6124447

SEQUENCE INFORMATION:

APPLICATING NATORI, SNUNJI

TITLE OF INVENTION: NOVEL ENZYME CATALYZING DEPHOSPHORYLATION

FILE REFERENCE: 32290-144753

CURRENT FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patent IN Ver. 2.0

SEQ ID NO 1

LENGTH: 724
                                                                                                                              53;
                                                                            Length 2516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 79; DB 4; Length 244; 24.0%; Pred. No. 0.72; ive 23; Mismatches 74; Indels
                                                                                                                            59; Indels
                                                                            DB 4;
                                                                       Query Match
10.5%; Score 80.5; Di
Best Local Similarity 22.4%; Pred. No. 14;
Matches 39; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                             61 SSNGVLRPAAPGGIANPEKKMNC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18465, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 EDGLSSNGVLRPAAPGGIANPEKKMNC-
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-18465
          ;
US-09-539-879A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-121-964-1
                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
```

엄

ò

g à

```
maltophilia
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Stenotrophomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.5<sup>1</sup>
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEX: SIGNAL
LOCATION: (1)...(41)
NAME/KEY: DOWALN
LOCATION: (196)...(290)
NAME/KEY: DOMAIN
                                                                                                                                                                                                        TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-071-035-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-408-647A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-408-647A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ⋧
                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 133-14, Application US/09071035
Sequence 134, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72; Indels 41; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 STKEA-----ANNGSAEKQSPAKNANPDDQANQVLNQLANMFPGQGLPQAILTSQTNNF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMN-CGTQCPN---SQNLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CGG-----SRADAIEPRYYESW----TRETESTWLTYTDSDALPSAAAT-DSGPEAG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGGKSTENTDSRSSAAESTTVESTKASAİKESSSK-AİTKSSDAKPSGTTİADSKATAS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 W--ATEAKRDAKRMS----AREVAINVTB-NIRQMD------RSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 LTAATTSQADQNNFRVLYYAEKEAIPVNDARVNQLTPISSFEKKTYGSDAEAKNAVN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.8%; Score 75.5; DB 4; Length 286; Best Local Similarity 27.1%; Pred. No. 2.3; Matches 48; Conservative 16; Mismatches 72; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                     APPLAICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
TELEFAX: (301) 309-8512
TELEFAX: (301) 309-8512
TELEFAX: (301) 309-8512
SEQUENCE CHARACTERISTICS:
TOWGTH: 286 amino acids
    COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT:
ATTORNEY/AGENT
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear; MOLECULE TYPE: protein US-09-071-035-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-071-035-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 -----NCG-----TQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 LVWSAATDNSGGSGVAGYDVYRNGSLVGSPSATQYTDGGLTASTAYTVRARDNAGNAS 278
                                                                                                                                                                                                                                                                            50 GLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMN-CGTQCPN---SQNLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                        79 STKEA-----ANNGSAEKQSPAKNANPDDQANQVLNQLANMFPGQGLPQAILTSQTNNF 132
                                                                                                                                          3 CGG-----SRADAIBPRYYESW----TRETESTWLTYTDSDALPSAAAT-DSGPEAG 49
                                                                                                                                                                                                           20 CGGGKSTENTDSRSSAAESTIVESTKASAIKESSSK-AIIKSSDAKPSGITIADSKAIAS 78
                                                                                                                                                                                                                                                                                                                                                                                                                      106 W--ATEAKRDAKRMS----AREVAINVTE-NIRQMD------RSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 ITAATTSQADQNNFRVLYYAEKEAIPVNDARVNQLTPISSFEKKTYGSDAEAKNAVN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 TWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGGLANPEKKM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                        41;
Query Match 9.8%; Score 75.5; DB 4; Length 305; Best Local Similarity 27.1%; Pred. No. 2.5; Matches 48; Conservative 16; Mismatches 72; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.8%; Score 75.5; DB 3; Length 700; 22.5%; Pred. No. 8.4; tive 15; Mismatches 58; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09408647A; Patent No. 639988; Batent No. 639888; GENERAL INFORMATION: APPLICANT: Kobayashi, Donald; TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas; TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas; TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas; TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas; TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas; FILE REFERENCE: Rut-Cook 98-0090; CURRENT FILING DATE: 1999-08-26; PRIOR PAPLICATION NUMBER: 60/098,036; PRIOR PLICHIO DATE: 1998-08-27; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2.
LENGTH: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (330) ... (483)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank No. 6399858 AF014950
DATABASE ENTRY DATE: 1997-09-23
```

2,

à g

```
Sequence 16753, Application US/09248796A

Sequence 16753, Application US/09248796A

Fatent No. 6747137

GENERAL INFORMATION:
FAPPLICATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR PAPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

RUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16753

LENGTH: 316
                  --TQKQNGLW 106
                                                        GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
TITLE OP INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29;
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-03-29;
PRIOR PILING DATE: 2000-02-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES CURAPATES C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 GDNATEAMKRDYESAKKKVEQSINLEKTVPEQSRDADVDASQGASAGGLPDLGSLLGGGL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CGTQCPNSQNLSSGPL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GSRADAIEPRYYESWIRETE-STWLTYT-----DSDALPSAAATDSG-PEAGGLHAGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Score 73.5; DB 4; Length 346; 29.4%; Pred. No. 5.2;
           52 HAGVLEDGLSSNGVLRPAAPGGIANPEKKMNC--GTOCPNSQNLSSGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YOR007C
US-09-538-092-723
                                                                                                                                                                                                  973 ASGSSASSIYFSSTDYASEVSENRORPODROR 1004
                                                                                                                                                     107 ATEAKRDAKRMSAREVAINVTEN-IROMDRSK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 EDGLSSNGVLRPAA-----PGGIANPEKKMN-
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 723, Application US/09538092
Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 29,45
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 TQKQNG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 LRNMAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-248-796A-16753
                                                                                                                                                                                                                                                                                                                                                                          US-09-538-092-723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                   g
                                                                                                                                                 δ
                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                           Sequence 8115, Application US/09328352
Patent No. 6562958
GARREAL INFORMATION:
GAPPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC99-03P8
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSA--AATDSG-----PEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGS-----RADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09618425

Batent No. 6475744

GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Reppert, David R.
APPLICANT: Jylka, Mark
APPLICANT: Jylka, Mark
APPLICANT: Jylka, Mark
APPLICANT: Stram, Sathyanarayanan
APPLICANT: Stram, Sathyanarayanan
APPLICANT: Stram, Sathyanarayanan
APPLICANT: Shaarman, Lauven
TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS WHICH
TITLE OF INVENTION: MODULATE CIRCADIAN RHYTHM
FILE REFERENCE: 00786-428010
CURRENT APPLICATION NUMBER: 60/03,005
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
PRIOR SPELICATION NUMBER: 60/133,33
PRIOR FILING DATE: 1999-07-22

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.6%; Score 74; DB 4; Length 1113; 25.0%; Pred. No. 25; ative 22; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.6%; Score 74; DB 4; Length 726; Best Local Similarity 33.8%; Pred. No. 13; Matches 26; Conservative 8; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GPQASGDPRSAAP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 VLEDGLSSNGVLRPAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Conservative
                                         |: :|:||
279 AQSGSISVT 287
119 AREVAINUT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus
US-09-618-425-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                           RESULT 11
US-09-328-352-8115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-618-425-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEC ID NO 9
```

엄 à

ઠે

```
51 LHAGVLEDGLSSNGVLRPA--APGGLANPEK-KMNCGT-----QCPNSQNLSSGPLTQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 EDGLSSNGVLRPAAPGGIANPEKKNNC-GTQCPNSQNL-SSGPLTQKQNGLWATEAKRD- 113
                                                                                                                                                    RESULT 15
US-09-496-320-11
; Sequence 11, Application US/09496320
; Batent No. 6593080
; GENERAL INFORMATION:
; APPLICANT: Smith, Alvin
; TITLE OF INVENTION: Infection in Humans
; TITLE OF INVENTION: Infection in Humans
; TITLE OF INVENTION: UNGER: US/09/496,320
; CURRENT APPLICATION NUMBER: US/09/496,320
; CURRENT FILING DATE: 2000-02-01
; EARLIER FILING DATE: 1999-02-01
; WUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GCGGSRADAIEPRYY-----ESWTRETESTWLTYTDSD---ALPSAAATDSGPEAGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Gaps
                                                                                    8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.5%; Score 73; DB 4; Length 512; Best Local Similarity 24.4%; Pred. No. 10; Matches 40; Conservative 17; Mismatches 57; Indels
                                    Query Match
9.5%; Score 73; DB 4; Length 316;
Best Local Similarity 34.7%; Pred. No. 5.2;
Matches 26; Conservative 9; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 KONGLWATEAKRDAKRMSAREVAINVTENIROMDRSKRVTKNCI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| | ::|:
-----QVDLGLRCWRHCL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 17, 2004, 15:30:04 Job time: 25.3333 secs
                                                                                                                                                                                                                                               | |: |: |
132 LLETKSTSSTTVSNN 146
                                                                                                                                                                                                                   114 ---AKRMSAREVAIN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 ROSRRWA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 512
; TYPE: PRT
TYPE: PRT
US-09-496-320-11
US-09-248-796A-16753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                        g
                                                                                                                                                                                                                   ò
```

```
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
```

1
mode
ΝS
ısing
ה ה
earch
38
oteir
brc
1
protein
ŏ

Title:	US-10-705-716A-8
Perfect score:	767
Sednence:	1 MGCGGSRADAIEPRYYESWTVTENIRQMDRSKRVT

KNCIN 145

2002273
parameters:
chosen
satisfying
hits
οĘ
number
otal

0	2000000000
length:	length:
sed	sed
DB	DB
Minimum	Maximum

*0	100%	45 summaries
Match	Match	first
Minimum	Maximum	Listing
Post-processing:		

Geneseq_23Sep04:* geneseqp1980s:*	eneseqp1990s	eneseqp2001s:	geneseqp2002s:* geneseqp2003as:*	eneseqp	deneredbz0048: *
4 :			 9 2		
Database					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	THE CONTON OF TOP OF THE		Ado48473 Rat PTH r	Aab95018 Human pro			Human	Brain	Нишап	Brain	_	2 Human	Mouse	Brain	Brain	Human	4 Brain	Adm46979 Brain and	Brain	Ado48482 PTH respo					Shrimn	Human h
SUMMARIES	AD048479	1001041	AD048473	AAB95018	AA019498	ABR58646	ADC31800	ADM46959	ADO48475	ADM46961	ADM46963	AD081902	ADO48481	ADM46962	ADM46960	ADO48477	ADM46964	ADM46979	ADM46977	ADO48482	AAR13456	ABB69330	ABP35624	ABG95028	AAG84930	ADJ70139
DB	įα	0	x	4	'n	v	۲	7	œ	^	7	'n	ထ	7	7	œ	7	7	7	ω	~	4	ហ	'n	4	7
Length	145	1 -	145	145	145	145	145	145	145	180	149	92	54	73	54	54	80	25	18	16	778	684	1433	574	1100	009
% Query Match	100 0		5.76	84.6	84.6	84.6	84.6	84.6	84.6	81.0	61.6	43.0	38.3	37.5	36.2	36.2	35.5	18.3	12.9	11.6	11.4	11.0	11.0	10.7	10.6	10.5
Score	767		0 7	649	649	649	649	649	649		472.5	329.5	294	288	278	278	272	140	66	68	87.5	84.5	84	82	81.5	80.5
Result No.		·	7	m	4	ഹ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adi40859 Human kin	Aam40296 Human pol	Aam40295 Human pol	Aam42081 Human pol	Aam42082 Human pol	Aau31506 Novel hum	Aaw01875 Neuronal	Aaw01884 Invertebr	Abb61076 Drosophil	_	_	Abb58571 Drosophil	Adj37991 D melanog	_	Abg15607 Novel hum	Abo69719 Pseudomon	Aay24750 Sarcophag	Aaw23327 Meripilus	Aau61325 Propionib	
AD140859	AAM40296	AAM40295	AAM42081	AAM42082	AAU31506	AAW01875	AAW01884	ABB61076	ABJ17935	AAU76758	ABB58571	ADJ37991	ABG09899	ABG15607	AB069719	AAY24750	AAW23327	AAU61325	ABM57844
643 8	852 4	872 4	886 4	886 4	974 4	2516 2	2516 2	2516 4	2516 5	516 3	108 4	108 7	260 4	592 4	244 7	724 2	396 2	121 4	121 6
80.5 10.5	80.5 10.5	80.5 10.5	10.5	10.5	10.5	10.5	10.5	10.5			0 10.4 1	-	10.4		10.3	10.2	10.1		10.0
26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; mouse; AD048479 standard; protein; 145 AA. Mouse PTH responsive gene protein. (first entry) 12-AUG-2004 AD048479; AD048479 

WO2004044152-A2. 27-MAY-2004. Mus sp. murine.

10-NOV-2003; 2003WO-US035655. 12-NOV-2002; 2002US-0425532P.

(AMHP ) WYETH.

Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ; WPI; 2004-420299/39. N-PSDB; ADO48478. New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.

Claim 9; SEQ ID NO 8; 169pp; English.

The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide;

```
determining whether an agent alters the expression of PAIGB mRNA;

c screening agents for effectiveness in altering expression of the nucleic

screening agents for effectiveness in altering expression of the nucleic

disorders; evaluating the efficacy of a treatment of a bone related

disorders; evaluating the effectiveness of treatment of a bone related

disorders in a subject; identifying polypeptides capable of binding to

PAIGS; monitoring the effectiveness of treatment of a subject with a bone

cralted agent; a transgenic animal comprising a first group of

animals composed of the transgenic animal and a second group of control

animals; studying bone mass determinants; studying the modulation of bone

cmass; studying an effect of PAIGS on bone disorders; identifying an agent

cmass; studying an effect of PAIGS on bone disorders; identifying an agent

cmass; studying an effect of PAIGS on bone disorders; identifying an agent

constructs, the first construct comprising a linked to a lub b binding domain

clinked to a lub binding domain which is linked to a nactivation domain

clinked to a pub binding domain which is onstruct comprising multiple copies of DNA, binding elements linked to a

minimal promoter which is linked to PAIGB cDNA, where upon the addition

construct comprising multiple copies of DNA binding elements linked to

minimal promoter which is linked to PAIGB cDNA, where upon the addition

conference whereapy. The PTH responsive gene may be

conference accorders by gene therapy. The mucleic acid is useful in

created disorders, e.g., osteoporasis. This sequence represents a PTH

creaponsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation;
transgenic animal; osteopathic; gene therapy; osteoporosis; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 767; DB 8; Length 145; Best Local Similarity 100.0%; Pred. No. 2.6e-78; Matches 145; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murrills RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robinson JA, Stojanovic-Susulic V, Babij P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO48473 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat PTH responsive gene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-420299/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADO48472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004044152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD048473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO48473
ID ADO4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
The invention relates to a novel PTH responsive gene (PAIGB) fragment construct comprising the isolated nucleic acid fragment operatively construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the construct construct; a vector comprising the nucleic acid fragment obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a nucleic acid fragment encoding the polypeptide; a method for chamming a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; composition for regulating bone-forming activity in a mannal comprising the nucleic acid fragment, polypeptide; or a mannal comprising the nucleic acid fragment; an antibody consent alters the expression of PAIGB gene or polypeptide; and gent that alters the expression of PAIGB gene or polypeptide; and gent that alters the expression of PAIGB gene or polypeptide; and gent that alters the expression of PAIGB menuleic caid fragment; screening for agents useful for treating bone related disorder in a subject; identifying polypeptides capable of binding to disorder; evaluating the efficacy of a treatment of a subject with a bone related agent, a transgenic animal comprising the DNA; an animal model for the study become mass determinants; studying the modulation of bone mass determinants; studying the modulation of bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an activation domain of the study of bone density and a stably transfected cell line comprising multiple copies of DNA binding elements linked to a DNA binding domain which is linked to an activation domain construct, comprising multiple copies of DNA binding elements linked to an activation domain along the promocer which is linked to a post the addition of PAIGB gene therapy. The PTH responsive gene may be preparing a composition for diagnosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SSNGVLRPAAPGGIANPEKKANCGTOCPNSONLSSGPLTOKONGLWATEAKRDAKKMSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                in
bone
                ic acid fragment encoding a PAIGB polypeptide, useful a composition for diagnosing, treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.3%; Score 746; DB 8; Length 145; 97.2%; Pred. No. 6.3e-76; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:16726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 EVALSVTENIRQMDRSKRVTKNCIN 145
                                            preparing a composition for diagnosing
related disorders, e.g., osteoporosis.
                                                                                                          Claim 9; SEQ ID NO 2; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB95018 standard; protein; 145 AA
                       New nucleic acid fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95018
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

m

```
EST; expressed sequence tag; colon cancer; stomach cancer; breast cancer; HS169395; HS127144; HS2; HS132793; HS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Describes and therapy of tumors, by determining expression rates of specific expressed sequence tags of the unigene cluster, and subsequently blocking their expression.
                                                                                                                                                                                                                                                                                                                                                                                                              (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
 AAO19498 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 5; 10pp; German.
                                                                                                                                                                                                                                                                                                                                    26-JAN-2001; 2001DE-01003694.
                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2001; 2001DE-01003694.
                                                                                                              HS1 protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-644836/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brett D, Kemmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAL50100.
                                                                                                                                                                                                                                                             DE10103694-A1
                                                                                                                                                                                                                          Unidentified
                                                                           20-DEC-2002
                                                                                                                                                                                                                                                                                                    01-AUG-2002.
                                      AA019498
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisentary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a for end sequence complementary to a
complementary strand of a polynucleotide which comprises a 5'-end sequence in a oligonucleotide comprises a 1'-end sequence, where the
complementary the primer sets can be used in antisense therapy and in
cypecification. The primer sets can be used in antisense therapy and in
cypecification. The primer sets can be used in antisense therapy and in
cypecification and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
complementary strand or diagnosis of the abnormality of the proteins encoded
condagance and any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
condagance of the appropriation of the complementary condagance of a condagance of the complementary condagance of a condagance of the complementary condagance of a condagance of the complementary condagance of the complementary condagance of the complementary condagance of the complementary condagance of the complementary condagance of the complementary complementary complementary complementary complementary complementary complementary complementary complementary complementary complementary complementary complementary complementary complementary complem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSNGVLRPAAPGGIANPEKKANCGTQCPNSQNLSSGPLTQKQNGLMATBAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PSNGVPRSTAPGGIPNPEKKTNCETOCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                     Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 16726; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 649; DB 4; Length 145; Pred. No. 6e-65; 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                 Saito K, Y, Otsuki T;
                                                                                                                                                                                                                                                                                                                 Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || ||||::|:|||||:|
EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                    Wakamatsu
                                                                                                                                                                                                                                                                                                         sogai T, Nishikawa T,
Sugiyama T, Wakamatsı
                                                                                                                                                                               27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%;
                                                                                                                           28-JUL-2000; 2000EP-00116126
                                                                                                                                                              99JP-00248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.6*
Best Local Similarity 83.4*
Matches 121; Conservative
                                                                                                                                                                                                                                                                            (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                 Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 145 AA;
                   Homo sapiens.
                                                    EP1074617-A2
                                                                                                                                                                29-JUL-1999;
                                                                                        07-FEB-2001
                                                                                                                                                                                                                                                                                                                                    တွ
                                                                                                                                                                                                                                                                                                               Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNAs.
                                                                                                                                                                                                                                                                                                                                  Ishii
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

3

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                              sequence
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solid
The present invention relates to the use of expressed sequence tags (ESTS), or variants, of the unigene cluster HS169395 (HS1), HS127144 (HS2) and/or HS132793 (HS3) for diagnosis and therapy of tumours, in which their expression rates in tumour cells and/or lymph nodes are determined. The EST sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with development of metastases); and for diagnosis and/or therapy of solid tumours, particularly of colon, stomach and breast. The present seque is a variant of the HS1 protein shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     84.6%; Score 649; DB 5; Length 145; 83.4%; Pred. No. 6e-65; ive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EVAINVIENIROMDRSKRVIKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR58646 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.4
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                   Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR58646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
ABR58646
ID ABR5
XX
AC ABR5
XX
DT 09-J
```

RESULT 4

ADC31800 standard; protein; 145 AA.

RESULT 6 ADC31800

```
The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-cegulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72660 represent cancer calated gene nucleotide sequences which encode the proteins given in ABRSBS231 to ABRSB709. Also described: [1] determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid, (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a patient by abhology, e.g. cancer (e.g. cancer of the bone marrow, colon/rectors, brain, breast, cervix, colon/rectormin, ischaemia, heart diseases, cervix, colon/rectormin, ischaemia, heart diseases, carrier of drug screening, particularly for identifying agents for treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRAPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New genes that are up-regulated or down-regulated in cancers, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                       Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.6%; Score 649; DB 6; Length 145; 83.4%; Pred. No. 6e-65; rive 10; Mismatches 14; Indels
                    Human cancer related protein SEQ ID NO:303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 753; 767pp; English.
                                                                                                                                                                                                                                                                                              2001US-0323887P.
2001US-0350666P.
2002US-0355145P.
2002US-0355257P.
                                                                                                                                                                                                                                                                                                                                                                                                                    (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                 2002US-0372246P.
                                                                                                                                                                                                                                        17-SEP-2002; 2002WO-US029560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 121; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-354600/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACC72796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 145 AA;
                                                                                                                                                           WO2003025138-A2
                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2002;
                                                                                                                                                                                                                                                                               L7-SEP-2001;
                                                                                                                                                                                                                                                                                                    20-SEP-2001;
                                                                                                                                                                                                                                                                                                                       13-NOV-2001;
                                                                                                                                                                                                                                                                                                                                       08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathologies
                                                                                                                                                                                                27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Afar D,
                                                       Human;
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                        Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; artiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antilicer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                      Wehrman T;
                                                                                                                                                                                                                                                                                                                                Weng G;
                                                                                                                                                                                                                                                                                                                      Wang J,
Wang Z, W
                                                     Human novel polypeptide sequence, SEQ ID NO:1882.
                                                                                                                                                                                                                                                                                                                    Ren F, Xue AJ, Zhao QA,
Wang D, Ma Y, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 1882; 1185pp; English.
                                                                                                                                                                                                                                                                                                                    Tang TY, Zhang J, Ren F, Xi
Zhou P, Ghosh M, Wang D, Mi
Haley-Vicente D, Drwanac RT;
                                                                                                                                                                                                                                                   24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                          24-SEP-2001; 2001US-0324631P.
                                                                                                                                                           gene therapy; chromosome 8.
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-371981/35.
N-PSDB; ADC30829.
                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                       WO2003029271-A2.
                                                                                                                                                                                  Homo sapiens.
                                 18-DEC-2003
                                                                                                                                                                                                                              10-APR-2003.
          ADC31800;
```

The invention relates to 971 novel human cDNA sequences (ADC29919-CADC3088) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the nucleic acid sequences over 99% identical with the nucleic acid of the invention; the crombinant production of a polypeptide of the invention; an antibody companies a polypeptide of the invention; an antibody compound which binds to a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention is amethods of perenting, treating or ameliorating a medical condition; kits computising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention invention methods for the identification of compounds that modulate the cypression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the colly sequences of the invention (ADC33394). The nucleic acids and polypeptides of the invention are textual in diagnostics, drug screening, forensics, gene mapping, in the contig for the invention are consecuted by the contigs (ADC33394). The nucleic acids and polypeptides of the invention are consecuted by the contigs (ADC33394). The nucleic acids and polypeptides of discases, Alzheimer's also used for treating diseases such as Parkinson's diseases or other caracting diseases such as Parkinson's diseases or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids may also be used as hybridisation probes or concer. The nucleic acids ma

9 9

Gaps ; 0

```
ö
                                                                                                                                                                                                                                   61 SSNGVLRPAAPGGIANPEKKMNCGTOCPNSQNLSSGPLTOKONGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                   are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                  9
                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Characterizing acute or chronic myelogenous leukemia, or prostate cancer
                                                                                                                                                                                                       1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                        Gaps
                                                                                                                                                      ;
0
                                                                                                                          DB 7; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brain and Acute Leukemia, Cytoplasmic alternate protein #1
                                                                                                                         ; Score 649; DB 7; Length 14; Pred. No. 6e-65; 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myelogenous leukemia; gene expression; BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 17; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                        || ||||:|:||||||:|
EVTINVIDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                       EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     ADM46959 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                          84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2004 (first entry)
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-441564/41.
N-PSDB; ADM46951.
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic; exon.
                                                                                               Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003040347-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                     Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ranner SM,
                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                  121
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                      ADM46959
  888888888
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                     ò
```

The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful

```
The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric consprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct, a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid cragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity; in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA; careening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related
                                                                                                                                                    ö
for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                            SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                   61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                        9
                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; PAIGB; bone-forming; bone; bone density modulation;
                                                                                                                                                                                  1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic animal; osteopathic; gene therapy; osteoporosis; human.
                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing related disorders, e.g., osteoporosis.
                                                                                                             DB 7; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murrills RJ;
                                                                                                         84.6%; Score 649; DB 7; Length 14
83.4%; Pred. No. 6e-65;
ive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babij P,
                                                                                                                                                                                                                                                                                                                                   EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                    || ||||::|:|||||:|
EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; SEQ ID NO 4; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robinson JA, Stojanovic-Susulic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AD048475 standard; protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PTH responsive gene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                         Query Match
Best Local Similarity 83.4
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-420299/39.
                                                                       Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADO48474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004044152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTH responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAY-2004
                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO48475;
                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             AD048475
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
 82666
                                                                                                                                                                                  à
                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
Liberiners; evaluating the effectiveness of treatment of a bone classical disponder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone crelated agent; a transgenic animal comprising the DNA; an animal model of or the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone cass; studying an effect of PAIGB on bone disorders; identifying whether an agent to for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain cellinked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparating a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLJQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acute myelogenous leukemia; gene expression; BAALC;
chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.6%; Score 649; DB 8; Length 145; 83.4%; Pred. No. 6e-65; ive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brain and Acute Leukemia, Cytoplasmic alternate protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM46961 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003040347-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanner SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM46961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윤
ò
```

```
ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
                                                                                                                              The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KIKAPTDSVSDEGLFSASKWAPLAVFSHCMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                        Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                         QCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNCIN
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-
                                                                                                                                                                                                                                                                                                                          DB 7; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain and Acute Leukemia, Cytoplasmic alternate protein #5.
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acute myelogenous leukemia, gene expression; BAALC
                                                                                                                                                                                                                                                                                                                        81.0%; Score 621.5; DB 7 67.2%; Pred. No. 1.1e-61; tive 10; Mismatches 14.
                                                                                                         Disclosure; SEQ ID NO 19; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM46963 standard; protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanner SM, De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                          Local Similaring
hes 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-441564/41.
N-PSDB; ADM46955.
WPI; 2003-441564/41.
N-PSDB; ADM46953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                              Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003040347-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM46963;
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM46963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

ä

19; Gaps

us-10-705-716a-8.rag

```
Disclosure; SEQ ID NO 21; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCPNSONLSSGPLTOKONGLWATE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCPNPQSLSSGPLTQKQNGLQTTE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2; 33pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHAN-) SHANGHAI BIODOOR GENE DEV
                               patient comprises assaying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ81902 standard; protein; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 61.6%;
l Similarity 65.3%;
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-2000; 2000CN-00125495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-2000; 2000CN-00125495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human dioxygenase 10.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-509506/55.
N-PSDB; ADQ81901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CN1344798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ81902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mao Y,
                               in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
ADQ81902
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; cobtaining a pulypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of fragment; an antibody that specifically binds to one or more epitopes of fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA; screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related
                                                                                                                                                                                                                                                                                                                           45 GPEAGGLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNG 104
     dioxygenase 10.12, polynucleotides encoding this polypeptide, a DNA recombination process to produce the polypeptide and antagonist against the polypeptide. The present invention also discloses the method of applying the polypeptide in treating various diseases, such as malignant tumours, inflammations, immunological diseases, haemopathy and HIV infection. The present sequence is the human dioxygenase 10.12.
                                                                                                                                                                                                                                                                                                                                                                        11 GPETGN------APGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                               Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murrills RJ;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse PTH responsive gene protein exon 2 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                         105 LWATEAKRDAKRMSAREVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                      Pred. No. 4.7e-29,
8; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babij P,
                                                                                                                                                                                                                               43.0%; Score 329.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 10; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robinson JA, Stojanovic-Susulic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO48481 standard; protein; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                      63.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-420299/39.
                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADO48480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004044152-A2.
                                                                                                                                                                               Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) WYETH
                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO48481;
                                                                                                                                                                                                                             Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp
                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO48481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8X888888
                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                      The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide human dioxygenase 10.12 and polynucleotides encoding this polypeptide, useful for treating various diseases, such as malignant tumors, inflammations, immunological diseases, hemopathy and HIV
       prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                      patient comprises assaying for the overexpression of one or more transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KIKAPTDSVSDEGLFSASKWAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GVLEDGLSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; enzyme; dioxygenase 10.12; malignant tumour; inflammation;
immunological disease; haemopathy; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention discloses a new kind of polypeptide, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
       or
Characterizing acute or chronic myelogenous leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 472.5; DB 7;
Pred. No. 6.1e-45;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO LTD.
```

```
disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PATGS; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA; an animal model of or the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying bone related disorders; identifying whether an agent of for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a linked to a DNA binding domain which allof which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a construct comprising multiple copies of DNA binding elements linked to a construct comprising multiple copies of DNA binding elements linked to a construct comprising multiple copies of DNA binding elements linked to a construct comprising multiple copies of DNA binding elements linked to a construct comprising multiple copies of DNA binding elements linked to a construct comprising multiple copies of DNA binding elements linked to of chemical inducer, transcription of PAIGB cDNA, where upon the addition of construct disorders by gene therapy. The nucleic acid is useful in preparating a composition for adagnosing, treating or preventing bone construct of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54 AA;
```

Gaps 54 54 1 MGCGGSRADAIEPRYYESWTRETESTWLIYTDSDALPSAAATDSGPEAGGLHAG 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG .. 0 Length 54; Indels Score 294; DB 8; I Pred. No. 2.3e-25; 38.3%; Scor. 100.0%; Pred. No. ... '... 0; Mismatches Query Match
Best Local Similarity 100.0 g ð

ö

ADM46962 standard, protein; 73 AA RESULT 13 ADM46962

ADM46962;

(first entry) 03-JUN-2004 Brain and Acute Leukemia, Cytoplasmic alternate protein #4.

myelogenous leukemia; prostate cancer; Brain and Acute Leukemia; acute myelogenous leukemia; gene expression; BAALC; Cytoplasmic; exon. chronic

sapiens Homo

'note= "encoded by GCS" Location/Qualifiers Key Misc-difference

WO2003040347-A2

15-MAY-2003.

12-NOV-2002; 2002WO-US036375

09-NOV-2001; 2001US-0348210P.

(OHIS ) UNIV OHIO STATE RES FOUND.

De La Chapell A; Tanner SM,

WPI; 2003-441564/41. N-PSDB; ADM46954.

Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.

Disclosure; SEQ ID NO 20; 78pp; English.

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                      leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acute myelogenous leukemia; gene expression; BAALC;
chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                    Characterizing acute or chronic myelogenous leukemia, or prostate cand in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of characterizing acute myelogenous
           The invention relates to a method of characterizing acute myelogenous
                                                                                                                                                                                                                                                                                                  1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLED
                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brain and Acute Leukemia, Cytoplasmic alternate protein #2
                                                                                                                                                                                                                              Length 73;
                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                            Score 288; DB 7;
Pred. No. 1.7e-24;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 18; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADM46960 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-2002; 2002WO-US036375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanner SM, De La Chapell A;
                                                                                                                                                                                                                              ch 37.5%;
1 Similarity 91.4%;
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-441564/41.
N-PSDB; ADM46952.
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003040347-A2
                                                                                                                                                                                              Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM46960;
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                               ADM46960
                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ************
                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                       g
```

```
The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprishing the nucleic acid fragment; containing a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA; correning agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treatment of a bone related disorders; evaluating the effectiveness of treatment of a bone related clisorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a bone ralated correlated agent: a transcoric animal comression the bone ariant and presented agents.
                                    36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                12-AUG-2004 (first entry)
                                                                   51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-420299/39.
                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADO48476.
Sequence 54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004044152-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-2004
                                                                                                                                                                                                                                                 ADO48477;
                                Query Match
                                                                   Matches
                                                                                                                                                                              RESULT 15
ADO48477
 g
                                                                                                                               g
                                                                                                                                                                                                                ò
```

related agent, a transgenic animal comprising the DNA, an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain

```
Job time
888888888888888
                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                         g
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                         PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; human.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.
                                                                                                     54
                                                                                                                                     54
                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murrills RJ;
                              Length 54;
                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                       Human PTH responsive gene protein exon 2 splice variant.
                            Score 278; DB 7;
Pred. No. 1.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robinson JA, Stojanovic-Susulic V, Babij P,
                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; SEQ ID NO 6; 169pp; English.
                                                                                                                                                                                                                             ADO48477 standard; protein; 54 AA.
```

```
ö
all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB CONA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                   Length 54;
                                                                                                                                                                                                                                                                                                                                                                                            36.2%; Score 278; DB 8; Length 54 94.4%; Pred. No. 1.5e-23; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 17, 2004, 15:22:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                Sequence 54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 99 secs
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

```
Sequence 20, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 35, Appl
Sequence 236244,
Sequence 180225,
Sequence 48905, A
                                                                                                                                                                                   (without alignments)
631.334 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30,
Sequence 19,
Sequence 21,
Sequence 20,
Sequence 18,
                                                                                                                                                       November 17, 2004, 15:22:38 ; Search time 81.3333 Seconds
                                                                                                                                                                                                                                                                                                                 1 MGCGGSRADAIEPRYYESWT.......VTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | / Gan2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| / Gan2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 US-10-293-239-17
4 US-10-177-390-30
4 US-10-293-239-19
4 US-10-293-239-19
4 US-10-293-239-21
4 US-10-293-239-18
4 US-10-293-239-18
4 US-10-293-239-37
4 US-10-293-239-37
7 US-10-293-239-35
7 US-10-293-239-35
6 US-10-425-115-236244
6 US-10-425-115-23624
6 US-10-767-701-48905
US-09-801-368-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1570615 seqs, 354127592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:
                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                US-10-705-716A-8
767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10:
11:
12:
13:
                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                649
472.5
472.5
288
272
272
140
888
888
888
888
888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
```

Sequence 112, App		Seguence 65588. A					equence	equence		Sequence 114095,		Sequence 180220,	Sequence 140197,	Sequence 14107, A	Sequence 8240, Ap	Sequence 43318, A	Sequence 336369,	Sequence 3926, Ap	Sequence 177907,	Sequence 158275,	Sequence 176, App	Sequence 176, App	Sequence 174, App	Sequence 174, App	Sequence 104701,	Sequence 46805, A	Sequence 339697,	16310		e 9815, A	Sequence 73164, A
US-10-149-310-112	US-10-425-115-275422	-10-425-114-65588	-10-	-10-424-599	-10 - 437 - 963	-10-156-761	US-10-408-765A-1945	1736	US-09-949-029-108	3	US-09-801-368-44	US-10-437-963-180220		US-10-156-761-14107		US-10-425-114-43318	ന		US-10-437-963-177907	US-10-437-963-158275	17	US-10-206-576-176		US-10-206-576-174	63-1	-767	-425-115-3	-437	-437-963-1	-739-93	US-10-282-122A-73164
15	17	15	16	15	16	14	16	16	10	16	σ	16	16	14	14	15	17	14	16	16	ο	14	σ		16					7	15
1433	264	274	609	455	1479	219	900	528	1108	966	876	1274	1491	670	268	320	422	426	391	276	286	286	305	305	373	167	360	604	296	479	580
11.0	ö	10.8	ö	10.7	10.7	10.6	10.5	10.4	10.4	0	0	0	10.2	0	О	10.0	10.0	10.0	6.6	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.7	7.6	7.6
84	82.5	82.5	82.5	82	82	81	80.5	80	80	79.5	79	78.5	78	77.5	77	76.5	76.5	76.5	92	75.5	75.5	75.5	75.5	75.5	75.5	75	75	75	74.5	74.5	74.5
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Publication No. US20030119043A1

SEQUENCE 17, Application US/10293239

Publication No. US20030119043A1

GENERAL INFORMATION:

APPLICANT: Tanner, Stephan

APPLICANT: de la Chapelle, Albert

APPLICANT: de la Chapelle, Albert

APPLICANT: de la Chapelle, Albert

TITLE OF INVENTION: BALLC expression as a diagnostic marker for acute leukemia FILE REFERENCE: 2272/04101

CURRENT APPLICATION NUMBER: US/10/293,239

CURRENT FILING DATE: 2002-11-09

RIOR RILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 17

LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SSNGVLRPAAPGGIANPEKKMANCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%; Score 649; DB 14; Length 145;
83.4%; Pred. No. 1.1e-59;
Live 10; Mismatches 14; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 83.4%
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-239-17
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-293-239-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Sequence 20, Application US/10293239
; Sequence 20, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
    APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
    TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; CURRENT ELLING DATE: 22727/04101
; CURRENT FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
                                                                                                                                                                                                          APPLICANT: Tanner, Stephan ApplicaNT: Tanner, Stephan APPLICANT: de la Chapelle, Albert TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia CURRENT APPLICATION NUMBER: US/10/293,239 CURRENT FILING DATE: 2002-11-12 PRIOR APPLICATION NUMBER: US 60/348,210 PRIOR FILING DATE: 2001-11-09 NUMBER OF SEQ ID NOS: 39 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KIKAPIDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKINCET 120
1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 -----GVLEDGLSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%; Score 288; DB 14; Length 73; llarity 91.4%; Pred. No. 2.7e-22; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 472.5; DB 14; Length
Pred. No. 3.4e-41;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ÓCPNPÓSLSSGPLTÖKÖNGLOTTE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCPNSONLSSGPLTQKONGLWATE
                                                                                                                                          ; Sequence 21, Application US/10293239; Publication No. US20030119043A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.3%
----hes 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-293-239-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-293-239-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 21
LENGTH: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR PLING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 QCPNSQNLSSGPLTQKQNGLMATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
                                                                                                                                                                                                                         of Eucaryotic Cells with Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GVLEDGLSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.0%; Score 621.5; DB 14; Length 180; Best Local Similarity 67.2%; Pred. No. 1.1e-56; Matches 121; Conservative 10; Mismatches 14; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

84.6%; Score 649; DB 14; Length 145;
Best Local Similarity 83.4%; Pred. No. 1.1e-59;
Matches 121; Conservative 10; Mismatches 14; Indels
                                                                                             Sequence 30, Application US/10177390

Publication No. US20030143743A1

GENERAL INPORMATION:

APPLICANT: Schiler, Gerold

TITLE OF INVENTION: Improved Transfection of Eucaryotic Cell

TITLE OF INVENTION: Polynucleotides by Electroporation

FILE REFERENCE: 021505wo/dH/ml

CURRENT APPLICATION NUMBER: US/10/177,390

CURRENT FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-293-239-19; Sequence 19, Application US/10293239; Publication No. US20030119043A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-293-239-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 19
LENGTH: 180
                                                                                    US-10-177-390-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-177-390-30
                                                                                                                                                                                                                                                                                                                                                                                               SEO ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

ij

85

0

ö

Gaps

.. 0

```
18.3%; Score 140; DB 14; Length 25; 100.0%; Pred. No. 2e-07; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         7 RADAIEPRYYESWTRETESTWLTYT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DAIEPRYYESWTRETEST 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 DAIEPRYYESWTRETEST 26
    SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 25
                                                                                                                                                                               Similarity 100.
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 18; Conservative
                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-293-239-35
                                                                                                                                                             Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                         GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT APPLICATION NUMBER: US 60/348,210
FRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOPTWARE: Patentin version 3.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/104101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR APPLICATION NUMBER: US 60/348,210
REAGE PRIOR ELING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BALC expression as a diagnostic marker for acute leukemia
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT APPLICATION NUMBER: US 60/348,210
PRIOR PRILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGCGCSRADAIBPRYXESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%; Score 278; DB 14; Length 54; 94.4%; Pred. No. 2e-21; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 272; DB 14; Length 80;
Pred. No. 1.4e-20;
1; Mismatches 2; Indels
                  Sequence 18, Application US/10293239
Publication No. US20030119043A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.3 Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-22
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 51; Conserv
US-10-293-239-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-293-239-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-293-239-37
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
US-10-236244
US-10-236244, Application US/10425115
Sequence 236244, Application US/10425115
Sequence 236244, Application US/10425115
Sequence 236244, Application US/10425115
Sequence 236244, Application No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFRENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369326
US-10-233-239-35

Sequence 35, Application US/10293239

Sequence 35, Application US/10293239

Publication No. US20030119043A1

APPLICANT: Tanner, Stephan

APPLICANT: Tanner, Stephan

TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia

FILE REFERENCE: 22727/04101

CURRENT APPLICATION NUMBER: US/10/293,239

CURRENT PILING DATE: 2002-11-12

PRIOR PILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 39

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

EBNGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
11.5%; Score 88; DB 17; Length 394;
Best Local Similarity 26.4%; Pred. No. 1.9;
Matches 39; Conservative 23; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%; Score 99; DB 14; Length 18; 100.0%; Pred. No. 0.0026; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i OTHER INFORMATION: Clone ID: MRT4577_147036C.1.pep
US-10-425-115-236244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Preq. w...
```

 $\overset{\diamond}{\circ}$ 

ઠ

```
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109212, 147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PLING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                927 LPPATTISLKPLFGSQSKNSLENRQRTPNVKR-----ENPEHEYLYGNDSNNNNNSEA 979
                                                                                                                                                                            36 LPSAAATDSGPEA----GGLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMNCGTQCPNS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 LPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSS
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                 91 QN-----LSSGPLTQKQ-NGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKR 138
                                                                                                                                                                                                                                                                                              80 DSCIGRWISTGISGHRPCSGLLSVQLLRQMPRSSAEQVRKEIKKQİQEQRRVRR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Maxon, Mary
APPLICANT: Sherman, Amir
TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
TITLE OF INVENTION: Zinc Binuclear Cluster Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     980 GHSPMTNTTNGNKRLKYEKDAKR-NAKDGGISKGENAHNFQNDTKKNMS 1027
                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 G--PLTQKQNGLWATEAKRDAKRMSAREVAINVTENIR--QMDRSKRVT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%; Score 84; DB 9; Length 1433; 29.4%; Pred. No. 26;
                                       Length 147;
                                                                                               46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Indels
                                          DB 16;
                                             Score 84; DB 1
Pred. No. 1.4;
                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milne, Todd
No. US20020128250Alman, Thea
Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 112, Application US/10149310; Publication No. US20040077039A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60, Application US/09801368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                               11.0%;
26.3%;
                                             Query Match
Best Local Similarity 26.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. US20020128250A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maxon, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
US-10-767-701-48905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-149-310-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-801-368-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-801-368-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEO ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENEKAL INFORMATION:
CHARACTURY: LA ROSA, Thomas J.
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Www. Wei
APPLICANT: Buckbaruk, Brad
APPLICANT: Buckbaruk, Brad
APPLICANT: Buckbaruk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
SURUM DISCASE
LENGTH: 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48905, Application US/10767701

Sequence 48905, Application US/10767701

Sequence 48905, Application US/10767701

Sequence 48905, Application US/10767701

Sequence 48905, Application No. US/10767701

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwid K.

APPLICANT: Cao, Yongwid K.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof For Plant Improvement

FIRE REFRENCE: 38-21 (53535) B

CURRENT PAPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                 90 SGGGPVTSGNGGERRPLFQRLWTEEDEIVILRGFAEFTAARGTAFASHQYDTDPFYEDMR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 TEEEWLAKFRKAASLQDAAHSSSGNGDRRGRGKKODGAPKEAQPKPANPGG-RNPGNC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 TESTWIT-YTDSDALPSAAATDSG-PEAGGLHAGVLEDGLSSNGVLRPAAPGGIANPEKK 80
                                  PSAAATDSGPEAGGLHAGVLEDG-LSSNGVLRPAAPGGIANPEKKMNCGTQCPN---SQN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.2%; Score 86; DB 16; Length 1597; Best Local Similarity 28.3%; Pred. No. 19; Matches 28; Conservative 10; Mismatches 41; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Clone ID: LIB3476-020-P1-K1-A12.pep
                                                                                                       ----AKRDAKRMSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_77610C.1.pep
US-10-437-963-180225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 MNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 REVAINVIEN--IROMDRSKRVIKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                              Sequence 180225, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                    93 LSSGPLTQKQNG-----LWATE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 48905
LENGTH: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                    q
                                                                                                                                                                                                                                                         g
```

```
US-10-425-115-275422
; Sequence 275422, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE REPERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 275422
; LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              927 LPPATTISLKPLFGSQSKNSLENRQRIPNVKR-----ENPEHBYLYGNDSNNNNNSEA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 LPSAAAIDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 DSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGGI---ANPEKKMNCGTQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 G--PLTQKQNGLWATEAKRDAKRMSAREVAINVTENIR--QMDRSKRVT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 34.4%; Pred. No. 4.3;
Matches 31; Conservative 8; Mismatches 32; Indels 19
                                                                                                                                                                                                                                                                                                                                                        Query Match 11.0%; Score 84; DB 15; Length 1433; Best Local Similarity 29.4%; Pred. No. 26; Matches 32; Conservative 15; Mismatches 50; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_182776C.1.pep
US-10-425-115-275422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- NSONLSSGPLTOKONG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 14184-019US1
CURRENT APPLICATION NUMBER: US/10/149,310
CURRENT FILING DATE: 2003-02-19
FRIOR APPLICATION NUMBER: PCT/US01/29288
FRIOR FILING DATE: 2001-09-19
FRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
LENGTH: 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 17, 2004, 15:48:54 Job time : 82.333 secs
                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-149-310-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
```

```
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

November 17, 2004, 15:00:21; Search time 19.6667 Seconds (without alignments) 709.395 Million cell updates/sec Run on:

US-10-705-716A-8 767

1 MGCGGSRADAIEPRYYESWT.......VTENIRQMDRSKRVTKNCIN 145 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	erythrocyte-bindin	genome polyprotein	CATB protein - vea	Ď		requlatory protein	conserved hypothet	hypothetical prote	elongation factor	probable quanine n	hypothetical prote		serotonin receptor	probable transport	period protein Per	hypothetical prote			tubulin alpha-2 ch	hypothetical prote	KCS1 protein - yea	ಗ	ALR protein - huma	ALR protein - huma	_		- 1	otubule-as	cytochrome-related
SUMMARIES	αI	A35970	GNVSSC	S54587	T43456	T03743	A57988	C69899	T37073	G90128	T09144	T41551	JE0301	S19156	AH0784	T14260	T02813	S61991	AG1028	S13337	H69775	S54640	T01383	T03455	T03454	T34418	G82962	T30250	T13564	C75521
	Length DB	778 2	365 1	1433 2				600 2	269 2	848 2	2559 2	781 2	516 2	645 2	601 2	1113 2	281 2	346 2	435 2	451 2	815 2	1050 2	424 2	4957 2	5262 2		652 2		5327 2	251 2
*	Query Match Le	11.4	11.0				10.3	10.2	10.2	10.1	10.1	10.0	6.6		.7	9.	9.	9.	9.6	9.5	9.5	'n	4.	4.	4.	m.	۳.	m.	۳.	.2
	Score	87.5	84	84	79.5	79.5	79	78.5	78	77.5	77.5	77	9/	92	74.5	7	73.5	73.5	73.5	72.5	72.5	72.5	72	72	72	71.5	71	71	71	70.5
	Result No.	н	7	М	4	S	9	7	œ	0	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25		27	28	29

## ALIGNMENTS

RESULT 1	
A35970	
erythrocyte-binding protein - Plasmodium knowlesi	nowlesi
C;Species: Plasmodium knowlesi	
C;Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text change 09-Jul-2004	Dec-1990 #text change 09-Jul-2004
C;Accession: A35970	
R; Adams, J.H.; Hudson, D.E.; Torii, M.; Ward,	R;Adams, J.H.; Hudson, D.E.; Torii, M.; Ward, G.E.; Wellems, T.E.; Aikawa, M.; Miller, L
Cell 63, 141-153, 1990	
A; Title: The duffy receptor family of plasmodi	A; Title: The duffy receptor family of plasmodium knowlesi is located within the microneme
A; Reference number: A35970; MUID:91004213; PMID:2170017	PMID:2170017
A;Accession: A35970	
A;Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-778 <ada></ada>	
A; Cross-references: UNIPROT: P22545; GB: M68518; GB: M37513: NID: 0160273: PID: 0160274	518; GB:M37513: NID:q160273: PID:q160274
C;Keywords: transmembrane protein	
Query Match 11.4%; Score 87.5;	.5; DB 2; Length 778;
TO.	
Marches 28; Conservative 13; Mismatches	cches 44; Indels 3; Gaps 3;
QY 31 TDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGV-LRPAAPGGIANPEKKMNC-GTQCP	GLSSNGV-LRPAAPGGIANPEKKMNC-GTQCP 88
:       OUT	TUSSINGSKISKISKISKISKISKISKISKISKISKISKISKISKIS
)	
QY 89 NSQNLSS-GPLTQKQNGLWATEAKRDAK 115	115
DD 412 DDKSQGSLGPHIDEKAILGEIHMEKDIE 439	439

Genome polyprotein - sugarcane mosaic virus (strain SC) (fragment)
N;Contains: carboxyl end of nuclear inclusion protein b; coat protein
C;Species: sugarcane mosaic virus, SCMV
C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004
C;Accession: PH0207
R;Frenkel, M.J.; Jilka, J.M.; McKern, N.M.; Strike, P.M.; Clark Jr., J.M.; Shukla, D.D.;
J. Gen. Virol: 72, 237-242, 1991
A;Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins on A;Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins on A;Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins on A;Title: Unexpected sequence genomic RNA
A;Title: Unexpected sequence protein; pMD1993866
A;Accession: PH0207
A;Residues: 1-365 <FRE>
A;Gross-references: UNIPROT:P25242; GB:D00948; NID:g222123; PIDN:BAM00796.1; PID:g222124
C;Superfamily: tobacco etch virus genome polyprotein
C;Superfamily: tobacco etch virus genome polyprotein
C;Superfamily: tobacco etch virus genome polyprotein
F;1-52/Product: nuclear inclusion protein b (fragment) #status predicted <IPB>
F;53-365/Product: coat protein #status predicted <COA>

11.0%; Score 84; DB 1; Length 365; 21.6%; Pred. No. 2.7; Query Match Best Local Similarity ŝ

3;

25;

```
bifocal protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 2-4 Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03743
R;Bahri, S.M.; Yang, X.Y.; Chia, W.
A;Bahri, S.M.; Yang, X.Z.; Chia, W.
A;Title: The Drosophila bifocal gene encodes a novel protein which colocalizes with activate on number: 215048; MUID:97415628; PMID:9271427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reaidues: 1-1063 < BAH>
A;Cross-references: UNIPROT:O16125; EMBL:AF011791; NID:g2388667; PIDN:AAB69991.1; PID:g
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 TIGSPSSSAN---ONPNPHLK---TKCKPGQSVAEGKPSAKE-----TIVDNSKS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDSEVSQSPAKNGSKPVHSNQHPQSPAVPPTYPSGPPPAASALSTTPGNNGVPAPAAPPS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 GIANPEKKOMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREVAINVTENIRQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory protein areA - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A57988; S10017; $70168; S72883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DSGPEAGGLHAGVLEDGLSSNGVLRPAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 NVTVTPIPKQRSSLLNTRSQEREMVRYILSESGERDGELESGEQPAGVVSNSRCGEVETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AGVLEDGLSSNGVLRPAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1063;
                                                                                                                                                                                                                                                                                                                                                                        Length 571;
                R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, December 1999
A;Reference number: Z22516
A;Accession: T43456
                                                                                                                                                                                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GSRADAIEPRYYESWIR-----ETESTWLTYTDSDAL---
                                                                                                                                                                                                           A,Cross-references: UNIPROT:075175; EMBL:AL133647
A,Experimental source: adult testis; clone DKFZp434L061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 ALGPKASPAPSHNSGTPAPYAQAVAPPAPSGPST 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: T03743
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GGIANPEKKMNCGTQCPNSQNLS----SGPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.4%; Score 79.5; D
Best Local Similarity 20.7%; Pred. No. 25;
Matches 39; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                               A, Note: DKFZp434L061.1
C, Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 TDSDALPSAAATDSGPEAGGLH-------
                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 79.5; 30.9%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: FlyBase: FBgn0014133
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cskTksis 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 MDRSKRVT 140
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                 A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-571 <AAA>
C; Accession: T43456
                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                         C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A57988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1433 <PEA>
A;Cross-references: UNIPROT:P39113; EMBL:Z49704; NID:g825540; PIDN:CAA89778.1; PID:g8255
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-302,'A', 304-767,'A',769-998,1003-1007,'S',1009-1015,'Q',1017-1018,'P',1020
A;Cross-references: EMBL:X94215; NID:g1122900; PIDN:CAA63906.1; PID:e214033; PID:g112290
A;Experimental source: strain ENY.WA-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              927 LPPATTTSLKPLFGSQSKNSLENRQRTPNVKR-----ENPEHEYLYGNDSNNNNSEA 979
                                                                                                                                                                63 NGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREV 122
                                                                                                                                                                                                                   79 QGGAQPPATGAAAQPPTTQ--GSQLPQGGATGGGGAQTGAGGTGSVTGGQRDKDVDAGTT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 LPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGGIANPEKKWNCGTQCPNSQNLSS 95
                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein DKFZp434L061.1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATB protein - yeast (Saccharomyces cerevisiae)
NiAlternate names: MSPB protein; protein YM8021.06c; protein YMR280c
CiSpecies: Saccharomyces cerevisiae
CiSpecies: OB-Jul-1995 #sequence revision 01-Sep-1995 #text_change 16-Aug-2004
CiAccession: S54587; S48234; $61595; S49498
                                                        5 GSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVL--EDGLSS
                                                                                    Molecule type: DNA
Residues: 1-746,'L',748-1433 <GRZ>
Cross-references: EMBL:X78344; NID:9559523; PIDN:CAA55139.1; PID:9559524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHSPMTNTTNGNKRLKYEKDAKR-NAKDGGISKGENAHNFQNDTKKNMS 1027
     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 G--PLTOKONGLWATEAKRDAKRMSAREVAINVTENIR--OMDRSKRVT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 84; DB 2; Length 1433; ; Pred. No. 13; 15; Mismatches 50; Indels
  80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: transmembrane protein
F;65-102/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F;456-472/Domain: transmembrane #status predicted <TM1>
F;738-754/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 13R
C;Superfamily: GAL4 zinc binuclear cluster homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Boles, E.; Hettmann, C.; Zimmermann, P.K. submitted to the EMBL Data Library, December 1995 A;Reference number: S61594
     23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: SGD:S0004893; MIPS:YMR280c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, March 1994 A;Reference number: S48234 A;Accession: S48234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Pearson, D.; Bowman, S. submitted to the EMBL Data Library, May 1995 A;Reference number: S54582 A;Accession: S54587
                                                                                                                                                                                                                                                                                                             137 GKITVPKLKAMSKKMRLPK 155
                                                                                                                                                                                                                                                                           123 AINVTENIROMDRSKRVTK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: SGD:CAT8; MSP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: S61595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simil
Matches 32; C
        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grzesitza, D.
        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                   ò
```

9

Gaps

67;

142

72

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chossion: C69899
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Nature 330, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, K.; A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucelly, M.; Cogiwara, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sckjouchi, J.; Sckowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tergefone, F.; Sckouch, K.; Yata, K.; Yoshida, K.; Vannets, P.; Winters, P.; Wipper, A.; Yamamoto, H.; Yamane, K.; Yata, K.; Yoshida, K.
                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P17429; EMBL:X52491; NID:q1019911; PIDN:CAA36731.1; PID:g115
A;Note: this sequence represents reinterpretation to include two exons
A;Accession: S10017
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: this sequence represents the authors' original translation R; Langdon, T; Sheerins, A; Ravagnani, A.; Gielkens, M.; Caddick, M.X.; Arst Jr., H.N. Mol. Microbiol. 17, 877-889, 1995
A; Title: Mirational analysis reveals dispensability of the N-terminal region of the Aspe A; Reference number: S70167; MUID:96123430; PMID:8596437
R;Kudla, B.; Caddick, M.X.; Langdon, T.; Martinez-Rossi, N.M.; Bennett, C.F.; Sibley, S.
EMBO J. 9, 1355-1364, 1990
                              EMBO J. 9, 1355-1364, 1990
A,Title: The regulatory gene areA mediating nitrogen metabolite repression in Aspergillu
A,Reference number: S10017; MUID:90228331; PMID:1970293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: nitrogen regulatory protein nit-2; GATA-type zinc finger homology ckeywords: DNA binding; transcription regulation; zinc finger F;670-723/Domain: GATA-type zinc finger homology <GZF> F;673-697/Region: zinc finger GATA motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645 ESGLNSAAPSRPASPGGTKNGEQNGPTTCTNCFTQTTPLWRRNPEGQPLCNACGLFLKLH 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-876 <CAD>
A; Cross-references: EMBL:X52491; NID:g1019911; PIDN:CAA36731.1; PID:g1154625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein yobL - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 ----PLTQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SSRVSK 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;MOLECULE type: DNA
A;Residues: 1-791,'A',793,'T',795,'SPGTNS',802-876 <LAN>
A;Cross references: EMBL:X52491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Description: mediates nitrogen metabolite repression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 EDGLSSNGVLRPAAPGGIANPEKK-----MNCGTQC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVVRPLSLK-----TDVIKKRNRNSANSLAVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.3%; Score 79; DB 1
28.4%; Pred. No. 22;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R, Caddick, M.X. submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S70168
A;Status: nucleic acid sequence not shown
                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
Residues: 1-876 <KUD>
A;Cross-references: UNIPROT:P17429; EMI
                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 158-876 <KU2>
A;Cross-references: EMBL:X52491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.48
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Reference number: S72883
A,Accession: S72883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
                                                                                                                                     A; Accession: A57988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 147/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: areA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
```

```
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The Complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: C69899
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Rolecule type: DMA
A; Rolecule type: DMA
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM>
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; Residues: 1-600 < KUM
A; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SCJ30.06c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 0.2 Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37073
R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9S1Y3; EMBL:AL109973; PIDN:CAB53301.1; GSPDB:GN00070; SCOEDI
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
A;Note: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G90128
B;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reli
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: G90128
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |: | : | : | | : | 394 AGKVINKASQAGKKIKDVKIPDLLPYNPKYKLALADNVPYNVUDSQNLKNELLTNAKKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 DAIBPRYYESWIRE-----IESTWLTYIDSDALPSAAAIDSGPEAGGLHAGVLEDGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SNGVLRPAAPGGIA-----NPEKKONCGTOCP----NSONLSSGPLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 ------QKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 DGTRKPFTGQKKSPPWLNKEKYD----AYEIEGKVKAKGKVKDVSRRV 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elongation factor EF-2 [imported] - Guillardia theta nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 78; DB 2; Length 269; 25.8%; Pred. No. 6.9; tive 10; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GGGVVTTGAGGGIV-PGEACRCGRAAHAPTNASMRS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SSNGVLRPAAPGGIANPEKKMNCG--TQCPNSQNLSS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%; Score 78.5; DB 2; 23.7%; Pred. No. 16; ive 22; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-269 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.8*
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 IEPRYYESWT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z21621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Gene: SCOEDB: SCJ30.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T37073
```

Ö

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-781 <MOO>
A;Coss.references: UNIPROT:074526; EMBL:AL023794; PIDN:CAA19355.1; GSPDB:GN00068; SPDB
A;Experimental source: strain 972h-; cosmid c70
C;Genetics:
A;Gene: SPDB:SPCC70.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inulinase (BC 3.2.1.7) - Aspergillus niger
C;Species: Aspergillus niger
C;Species: Aspergillus niger
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: JE0301
R;Ohta, K.; Akimoto, H.; Matsuda, S.; Toshimitsu, D.; Nakamura, T.
Biosci. Biotechnol. Biotechnem 62, 1731-1738, 1998
A;Title: Molecular cloning and sequence analysis of two endoinulinase genes from Asperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-516 cOHTP-
A;Cross-references: UNIPROT:074641; UNIPROT:Q8X217; UNIPROT:Q96WZ8; UNIPROT:074642; DDB
C;Superfamily: Penicillium purporogenun inulinase
C;Reywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 YESWPHSTEPDMFTYAVSGSLKLTPQGTGFDCINPANPFSPGYSGKSSMKSDDNVGSSAN 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRPAAPGGIANPEKKMNCG-TQCP--NSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 YESWIRETESTWLIYIDSDAL---PSAAATDS-----GPEAGGLHAGVLEDGLSSNGV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerotonin receptor 2B - fruit fly (Drosophila melanogaster)
NiAlternate names: 5-hydroxytryptamine receptor 2B (5-HTR2B)
CiSpecies: Drosophila melanogaster C; Species: Drosophila melanogaster C; Species: Drosophila melanogaster C; Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004 C; Accession: 519154 #sequence_revision N: Plassat, J.L.; Hen, R. Ex; Saudou, F.; Boschert, U.; Amlaiky, N.; Plassat, J.L.; Hen, R. EMBO J. 11, 7-17, 1992
                                                                                                                                                                                               Cispecies: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                           hypothetical protein SPCC70.05c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQTVINYTQSNATLSVDRTESGDISYDPAAGGVHTAKLEEDGTGLVSIRVL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 TESTWLTYTDSDALPSAAATDSG----PEAGGLHAGVLED---GLSSNGVL
                                                                                                                                                                                                                                                                             10.0%; Score 77; DB 2; Length 781; llarity 26.6%; Pred. No. 30; Conservative 16; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.9%; Score 76; DB 2; Length 516;
12.3%; Pred. No. 23;
[ve 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 42.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AINVTENI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 LVDETKDM 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T41551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JE0301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: rhoGEF2
A;Cross rhoGEF2
A;Cross rhoGEF2
A;Cross rhoGEF2
A;Note: orchestrates cell shape changes during gastrulation
C;Function: mediates actin rearrangements required for cell shape changes during gast C;Superfamily: rat Munc13-3 protein; protein kinase C zinc-binding repeat homology
C;Keywords: embryo; GTP exchange; signal transduction
F;1151-1200/Domain: protein kinase C zinc-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-676, L', 678-837, L', 839-889, 'S',891-1243, 'D',1245-1358, 'E',1360-1368, 'R',1
A;Cross-references: EMBL:AF032870; NID:g2760367; PIDN:AAC38820.1; PID:g2760368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable guanine nucleotide exchange factor RhoGEF2 - fruit fly (Drosophila melanogaster N,Alternate names: Shar pei/DRhoGBF2
C;Species: Drosophila melanogaster
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                   A;Genome: nucleomorph
C;Superfamily: translation elongation factor 2; translation elongation factor Tu homolog
C;Keywords: nucleomorph
A;Residues: 1-848 <DOU>
A;Cross-references: UNIPROT:Q98S60; GB:AF083031; NID:g13794345; PIDN:AAK39722.1; GSPDB:CGenetics:
A;Gene: EF2
A;Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2559 <4ABS>
A;Residues: 1-2559 <4ABS>
A;Coses-references: UNIPNOT:044113; EMBL:AF031930; NID:g2687355; PID:g2687356
B;Barrett, K.; Leptin, M.; Settleman, J.
Cell 91, 905-915, 1997
A;Title: The Rho GTPase and a putative RhoGEF mediate a signaling pathway for the cell A;Reference number: Z16618; MUID:98088790; PMID:9428514
A;Accession: T09223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 799 GSSPDNMHPRHPDRITKTTSGSW-EIVEKDGESSPPGTPPPPYLSSSHMTVLEDPNENNR 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 AVEPKNPSDLPKLIEGL-KRLSKSDPLVQCMTEESGEHIVAGAGELHLEICLKDLQDDFM 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SNGVLRPAAP-----GGIANPEKKMNCGTOCPNSQN---LSSGPLTQKQNGLWATEA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |: : | : : | : | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPE----AGGLHAGV----LEDGLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858 GAAAAGPGVFIESHQ-----FTPWAGASSPIPISLHSNHMHAAQSNDTQKEIISME 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 VLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSARE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 77.5; DB 2; Length 2559; 23.9%; Pred. No. 1.1e+02; ive 16; Mismatches 66; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 KRDAKRMSAREVAINVTENIROMDRSKRVTK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | : | : | : | 607 IDDGKIKSSDEPKTRIKELKQKFDMNEEDIK 637
                                                                                                                                                                                                                                                                                                                                                                                                               Match 10.1%; Score 77.5; DB Local Similarity 25.2%; Pred. No. 30; les 38; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 11-Jun-1999 #sequence_revision 11-Jun-199
C;Accession: T09144; T09223
R;Haecker, U.; Perrimon, N.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z16586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.9%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T09144
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

5

Gaps

99

ŝ

```
Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: Per3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable transport system periplasmic binding protein STY2452 [imported] - Salmonella en Cispecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0784
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
Title: A family of Drosophila serotonin receptors with distinct intracellular signalli Reference number: S19155; MUID:92155185; PMID:1310937
                                                              A; Molecule type: mRNA
A; Residues: 1.645 < c&AU>
A; Cross-references: UNIPROT:P28286; EMBL:Z11490; NID:97506; PIDN:CAA77571.1; PID:97507
C; Genetics:
A; Gene: FlyBase:5-H71B
A; Cross-references: PlyBase:FBgn0004572
C; Superfamily: octopamine receptor type I
C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane #status predicted < TML>
F; 124-145/Domain: transmembrane #status predicted < TML>
F; 133-214/Domain: transmembrane #status predicted < TM4>
F; 234-256/Domain: transmembrane #status predicted < TM4>
F; 234-256/Domain: transmembrane #status predicted < TM4>
F; 264-587/Domain: transmembrane #status predicted < TM6>
F; 264-587/Domain: transmembrane #status predicted < TM6>
F; 297-619/Domain: transmembrane #status predicted < TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AL513382; PIDN:CAD02598.1; PID:g16503454; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:|:| |: | : | 342 FYNAWSRTNSYFQNTEYAARNYPDADELVLLAPMKKDLPPEVFTQIYQPPVSNG----- 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 EDGLSSNGVLRPAA----PGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | :| :| | | :| 396 -DGYDRENLLKADALLTQAGWVINGQQRVNSVTGKPLTFELL---LPASSNSQWVLPFQH 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 TYTDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGG----IANPEKKMNCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LPSAAATD--SGPEAGGLHAGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%; Score 76; DB 2; Length 645; 31.0%; Pred. No. 30; ive 12; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 TQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREVAI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: periplasmic oligopeptide-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 38; 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.7%; Score 74.5; 22.8%; Pred. No. 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 YYESWTR-----ETESTWLTYTDSDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|
NLQR-----LGITMTIRQVDNSQ 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 DAKRMSAREVAINVTENIRQMDRSK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.0.
Thes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-601 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: AH0784
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: STY2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ⋧
```

RESULT

```
period protein Per3 - mouse

() Species: Mus musculus (house mouse)

() Species: Mus musculus (house mouse)

() Accession: T14260

R;Zylka, M.J.; Shearman, L.P.; Weaver, D.R.; Reppert, S.M.

Neuron 20, 1103-1110, 1993

A;Title: Three period homologs in mammals: differential light responses in the suprachia. A;Title: Three period homologs in mammals: pMID:9655499

A;Accession: T14260

A;Accession: T14260

A;Actus: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Retus: preliminary;

A;Actus: preliminary;

A;Actus: Careferences: UNIPROT:070361; EMBL:AF050182; NID:g3136149; PID:g3136150; PIDN:AAC4

C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 HAGVLEDGLSSNGVLRPAAPGGIANPEKKMNC--GTQCPNSQNLSSGPL---TQKQNGLW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         860 LGAAGSSELAPLVPAMAPNPEPTTSGHSQRRVENWEAH--SEELPFISSRSSP---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGS------RADAIEPRYYESWIRETESTWLIYTDSDALPSAAATDSGPEAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 9.6%; Score 74; DB 2; Length 1113; Local Similarity 25.0%; Pred. No. 87; Onservative 22; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          973 ASGSSASSIYFSSTDYASEVSENRORPODROR 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 ATEAKRDAKRMSAREVAINVTEN-IROMDRSK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 17, 2004, 15:28:55
Job time : 21.6667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: circadian rhythm
```

```
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                 Copyright
```

- protein search, using sw model OM protein

November 17, 2004, 14:58:39; Search time 98 Seconds (without alignments) 530.773 Million cell updates/sec Run on:

US-10-705-716A-2

Title: Perfect score:

1 MGCGGSRADAIEPRYYESWT......VIENIRQMDRSKRVTKNCIN 145 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB & Maximum DB &

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

genesemp2000s:\*
genesemp2001s:\*
genesemp2002s:\*
genesemp2003as:\* A Geneseq 23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

# SUMMARIES

בנים	Description	Ado48473 Rat PTH	MOU		HS1 D1		Human	Brain	Human	Brain	Brain	Human	Mouse		Brain	Human	Brain		Adm46977 Brain and	Aar13456 Duffy rec	PTH re		Novel	Protei	-	
COLUMN TO COLUMN	ID	AD048473	AD048479	AAB95018	AA019498	ABR58646	ADC31800	ADM46959	AD048475	ADM46961	ADM46963	ADQ81902	ADO48481	ADM46962	ADM46960	AD048477	ADM46964	ADM46979	ADM46977	AAR13456	AD048482	ABG09899	ABG15607	ABU17344	ADA36828	AAE25052
	DB		æ	4	'n	9	7	7	æ	7	7	Ŋ	ထ	7	7	œ	7	7	7	~	œ	4,	4	9	9	Ŋ
	Length DB	145	145	145	145	145	145	145	145	180	149	92	54	73	54	54	80	25	18	778	16	260	592	718	726	700
do	Query Match	100.0	97.3	84.1	84.1	84.1	84.1	84.1	84.1	80.5	61.7	43.7	38.3	37.5	36.2	36.2	35.5	18.3	12.9	12.1	11.6	11.4	11.4	11.0	11.0	10.9
	Score	767	746	645	645	645	645	645	645	617.5	473.5	335.5	294	288	278	278	272	140	66	92.5	83	87.5	87.5	84	В	83.5
	Result No.	Н	2	e	4	Ŋ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25

Abp35624 Fungal ZB Aae14866 S. clavul Adi70139 Human hea		Human Novel	Novel Shrimp	Aay00097 Enterococ Abp43316 E faecali Abu88344 E. faecal	Brt	Abp43315 E faecali Abu88343 E. faecal	Abul3594 Enterococ Abj37782 Human tum
ABP35624 AAE14866 ADJ70139	AAM40296 AAM40295 AAM42081	AAM42082 AAU31506 ABG21379	ABG15431 AAG84930	AAY00097 ABP43316 ABU88344	ABU13595 AAY00096	ABV83315 ABV88343	ABU13594 ABJ37782
9 6 9	4 4 4	4 4 4	44	0 W	9 71	o 0	9 9
1433 339 600	852 872 886	986 974 275	275	286 286 286	305	305	305 661
10.8 10.7 10.6	10.6 10.6	10.6	10.5	1001	10.4	10.4	10.4
83 82 81.5	81.5 81.5 81.5	81.5 81.5 80.5	80.5	79.5 79.5	79.5	79.5	79.5
26 27 28	29 30 31	3 3 3 4 3 2	36	337 398	4 4 4 0 L 0	4 4 5	4 4 5

## ALIGNMENTS

RESULT 1

ADO48473 standard; protein; 145 AA. Rat PTH responsive gene protein. (first entry) 12-AUG-2004 ADO48473; AD048473 

PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; rat.

Rattus sp.

WO2004044152-A2.

27-MAY-2004.

10-NOV-2003; 2003WO-US035655.

12-NOV-2002; 2002US-0425532P.

(AMHP ) WYETH.

Murrills RJ; Babij P, Robinson JA, Stojanovic-Susulic V,

WPI; 2004-420299/39. N-PSDB; ADO48472.

New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.

Claim 9; SEQ ID NO 2; 169pp; English.

The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively chimed to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA;

cc screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone cass; studying an effect of PAIGB on bone disorders; identifying an agent of for treating activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain construct to but by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a nativate by a constitutive promoter, the second construct which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB colymucleotide has osteopathic activity. The PPH responsive gene may be compensing a composition for diagnosing, treating or preventing bone corpused disorders, e.g., osteoporosis. This sequence represents a PTH creaponsive gene protein of the invention. 8888888888888888888888888888888

Sequence 145 AA;

```
61 SSNGVLRPAAPGGIANPEKKWNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                  1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
                                                                                       1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
                                 Gaps
                                 ö
100.0%; Score 767; DB 8; Length 145; 100.0%; Pred. No. 3.9e-76;
                                 Indels
                                   ..
                              0; Mismatches
                                                                                                                                                                                                          121 EVAISVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                          121 EVAISVTENIROMDRSKRVTKNCIN 145
                                     Matches 145; Conservative
 Query Match
Best Local Similarity
                                                                                                                                                                                                          ð
                                                                                                     a
                                                                                                                                                                         셤
                                                                       à
                                                                                                                                         à
```

```
PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
                 ADO48479 standard; protein; 145 AA.
                                                                          Mouse PTH responsive gene protein.
                                                                                                                                                                                       10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                         12-NOV-2002; 2002US-0425532P
                                                       12-AUG-2004 (first entry)
                                                                                                                                                   WO2004044152-A2.
                                                                                                                                                                      27-MAY-2004.
                                     AD048479;
                                                                                                                                 Mus sp.
                                                                                                                murine
RESULT 2
         ADO48479
```

The invention relates to a novel PTH responsive gene (PAIGB) fragment concoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively comprehensive per construct, a vector comprising the nucleic acid fragment in the construct, a vector comprising the nucleic acid fragment; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of tragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody conference of the nucleic acid fragment, sortening the expression of PAIGB man.

CC determining whether an agent alters the expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorders; evaluating the efficacy of a treatment of a bone related disorders; evaluating the efficacy of a treatment of a subject with a bone contraining the efficacy of a treatment of a subject with a bone for the study of bone density modulation comprising the DMA, an animal model cor the study of bone density modulation comprising a first group of control animals composed of the transgenic animal and a second group of control mass; studying an effect of paice of pAIGB on bone disorders; identifying whether an agent which the bone for which is linked to an activation domain which is linked to an activation domain which is linked to an activation domain which is linked to an activation domain with the pance forming activity; and a stably transfected cell line constructs comprising multiple copies of DMA binding elements linked to a mathematical parameter of entirely man and parameter of entirely and parameter of entirely man and parameter of ent of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polymucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. related disorders, e.g., osteoporosis. Th responsive gene protein of the invention. Claim 9; SEQ ID NO 8; 169pp; English 

1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 0; Gaps DB 8; Length 145; Pred. No. 8e-74; 2; Mismatches 2; Indels 97.3%; Score 746; 97.2%; Pred. No. 8 Matches 141; Conservative Similarity Query Match Best Local S

Sequence 145 AA;

0

9 1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR g ð g

EVALSVIENIROMDRSKRVIKNCIN 145 121 EVAINVTENIRQMDRSKRVTKNCIN 145 AAB95018 standard; protein; 145 AA 121 AAB95018; RESULT 3 **AAB**95018 X X X X X X X X X X ò

Human; primer; detection; diagnosis; antisense therapy; gene therapy. Human protein sequence SEQ ID NO:16726.

(first entry)

26-JUN-2001

Murrills RJ;

Stojanovic-Susulic V, Babij P,

AMHP ) WYETH. Robinson JA, WPI; 2004-420299/39. N-PSDB; ADO48478.

AAO19498 standard; protein; 145 AA

20-DEC-2002

AA01949B;

```
The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification, Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the conjugate comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprises an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 -end sequence, where the complement of an oligonucleotide comprises a 3 -end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, centured and sequences are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13633 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13639 represent human amino acid sequences and the expe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID NO 16726; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 645; DB 4; Length 145; Pred. No. 1.1e-62; 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K, Y, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || |:||:||:|||||:|
EVTINVIDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVALSVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                           sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                       27-AUG-1999; 99JP-00300253.
11-JAN-22000; 2000JP-00118776.
02-MAY-2000; 2000JP-0018776.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                   28-JUL-2000; 2000EP-00116126.
                                                                                                                                                                                                                        99JP-00248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.4%
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                              (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 145 AA;
                           Homo sapiens
                                                                      EP1074617-A2
                                                                                                                                                                                                                   29-JUL-1999;
                                                                                                                      07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
AA019498
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
ö
                                                                                                                            HS1; variant; cancer; tumour; unigene cluster; cytostatic; metastasis;
EST; expressed sequence tag; colon cancer; stomach cancer; breast cancer;
HS169395; HS127144; HS2; HS132793; HS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by determining expression rates of of the unigene cluster, and subsequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYXESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the use of expressed sequence tags (BST8), or variants, of the unigene cluster HS169395 (HS1), HS127144 (HS2) and/or HS12793 (HS3) for diagnosis and therapy of tumours, in which their expression rates in tumour cells and/or lymph nodes are determined. The BST sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with adevelopment of metastases); and for diagnosis and/or therapy of solid tumours, particularly of colon, stomach and breast. The present seque is a variant of the HS1 protein shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.1%; Score 645; DB 5; Length 14:
83.4%; Pred. No. 1.1e-62;
ive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVAISVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR58646 standard; protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosis and therapy of tumors, specific expressed sequence tags blocking their expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 5; 10pp; German.
                                                                                                                                                                                                                                                                                        26-JAN-2001; 2001DE-01003694.
                                                                                                                                                                                                                                                                                                                        26-JAN-2001; 2001DE-01003694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.4%
Matches 121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Brett D, Kemmner W;
                                                                                              HS1 protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-644B36/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAL50100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 145 AA;
                                                                                                                                                                                                                          DE10103694-A1
                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                           01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR58646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
ABR58646
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXXXX
```

9 9 Human novel polypeptide sequence, SEQ ID NO:1882.

(first entry)

18-DEC-2003 ADC31800;

ADC31800 standard; protein; 145 AA.

RESULT 6

ADC31800

```
The present any of the genes that are up-regulated or down-
comparises the sequence of any of the genes that are up-regulated or down-
comparises the sequences (e.g. about 1031 genes up-regulated in
caute lymphocytic leukemia). Acc72641 to Acc72660 represent cancer
related gene mucleotide sequences which encode the proteins given in
ABR58521 to ABR58709. Also described: (1) determining the presence or
cabsence of a pathological cell in a patient; (2) an expression vector
comparising the vector; (4) an isolated polypeptide, which is encoded by
comprising the vector; (4) an isolated polypeptide, which is encoded by
comprising the vector; (5) an antibody that appecifically binds the polypeptide
of (4); (6) specifically targeting a compound to a pathological cell in a
cut general gassay. The nucleic acid is useful sex charageus:
therapeutic targets. In particular, the nucleic acid is useful for
charapeutic targets. In particular, the nucleic acid is useful for
charapeutic paragets, cervix, colon/rectum, kidney, lung, owary,
bladder, brain, breast, cervix, colon/rectum, kidney, lung, owary,
characcas, prostate, skin and uterus), wounds, ischaemia, heart disease,
atherosclerosis and endometriosis. The nucleic acid is also useful in
charactering the paticularly for identifying agents for treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes an isolated nucleic acid molecule, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDALPSAAAIDSGPEAGGLHAGVLEDGP
                                                            cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.1%; Score 645; DB 6; Length 145; 83.4%; Pred. No. 1.1e-62; Live 10; Mismatches 14; Indels
                                                                                     disease; atherosclerosis; endometriosis.
                    Human cancer related protein SBQ ID NO:303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 753; 767pp; English.
                                                                                                                                                                                                                                                                                                                    20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
08-FEB-2002; 2002US-035145P.
08-FEB-2002; 2002US-035557P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                          17-SEP-2002; 2002WO-US029560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-354600/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACC72796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 145 AA;
                                                                                                                                                                       WO2003025138-A2
                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                     17-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathologies
                                                                                                                                                                                                                27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Afar D, Az
Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                              Human;
                                                                                       heart
```

```
The invention relates to 971 novel human cDNA sequences (ADC29919-CADC3089) and the polypeptides they encode (ADC30890-ADC31860). The ADC30899 and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid of the invention, it the the nucleous and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody companies a polypeptide of the invention; and methods of compound which binds to a polypeptide of the invention; and methods of compounds of compound which binds to a polypeptide of the invention. The invention further discloses methods of perenting, treating or ameliorating a medical condition; kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention methods for the identification of compounds that modulate the expression or activity of the polymucleotide and/or polypeptide; and 767 contig sequences corresponding to the cONA sequences of the invention contig sequences corresponding to the cONA sequences of the invention of contigs equences corresponding to the cONA sequences of the invention consectual in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's diseases or cancer. The nucleic acids may also be used as Hybridisation probes or cancer. The nucleic acids may also be used as Hybridisation probes or cancer. The nucleic acids may also be used as Hybridisation probes or cancer. The nucleic acids may also be used as Hybridisation probes or cancer. The nucleic acids may also be used as Hybridisation probes or cancer. The nucleic acids may also be used as Hybridisation probes or cancer. The nucleic acids may also be used as Hybridisation probes or cancer. The nucleic acids may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                  Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; monlecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F, Xue AJ, Zhao QA, Wang J, Wehrman
Wang D, Ma Y, Asundi V, Wang Z, Weng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 1882; 1185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haley-Vicente D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-2001; 2001US-0324631P.
                                                                                                                                                                                                                                                                                                                                                         gene therapy; chromosome B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-371981/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang TY, Zhang J,
Zhou P, Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADC30829
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003029271-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer.
```

SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120 

61

d ð 셤

EVALSVTENIROMDRSKRVTKNCIN 145

121 121

g à

1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL

9 9

Gaps . 0

0

60 9 120

```
PSNGVPRSTAPGGIPNPEKKTNCETÓCPNPOSLSSGPLTOKONGLOTTEAKRDAKRMPAK 120
are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypebtide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Characterizing acute or chronic myelogenous leukemia, or prostate cancer
                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                    61 SSNGVIRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR
                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                       .;
0
                                                                                                                                                        Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brain and Acute Leukemia, Cytoplasmic alternate protein #1
                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acute myelogenous leukemia; gene expression; BAALC;
                                                                                                                                                    84.1%; Score 645; DB 7;
83.4%; Pred. No. 1.1e-62;
                                                                                                                                                                                    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                        || |:||:|:|||||:|
EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                      EVAISVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM46959 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-2004 (first entry)
                                                                                                                                                                                    Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-441564/41.
N-PSDB; ADM46951.
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                   Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003040347-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanner SM,
                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                    Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
   888888888
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                g
```

```
The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment is obtaining a polypeptide, detecting the presence of the nucleic acid fragment; containing a polypeptide, detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA; screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related
                                                                                                                                                                ö
for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and \theta.
                                                                                                                                                                                                                                                                              SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                   61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                       9
                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; human.
                                                                                                                                                                                                 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.
                                                                                                                                                                ó
                                                                                                                        Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murrills RJ;
                                                                                                                                                              14; Indels
                                                                                                                    84.1%; Score 645; DB 7;
83.4%; Pred. No. 1.1e-62;
ive 10; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babij P,
                                                                                                                                                                                                                                                                                                                                                                               || |:||::|:|||||:|
121 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                               EVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; SEQ ID NO 4; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robinson JA, Stojanovic-Susulic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO48475 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PTH responsive gene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry
                                                                                                                                       Best Local Similarity 83.4
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-420299/39.
                                                                            Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004044152-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADO48474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-2004.
                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD048475;
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD04847
  SSSSS
                                                                                                                                                                                                 à
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                           ò
```

```
disorder in a subject; identifying polypeptides capable of binding to disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DMA; an animal model of for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a light binding domain call of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a linked to a disorders, the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be caped disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWIRETESTWLIYIDSDALPSAAAIDSGPEAGGLHAGVLEDGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWIRETESTWLIYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brain and Acute Leukemia, Cytoplasmic alternate protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute myelogenous leukemia; gene expression; BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 645; DB 8;
; Pred. No. 1.1e-62;
10; Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by GCS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVAISVTENIRQMDRSKRVTKNCIN 145
 efficacy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM46961 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                        84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2004 (first entry)
disorders; evaluating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003040347-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanner SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM4696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
ή;
                                                                                                                                     The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAMLC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAMLC overexpression. This sequence corresponds to a BAMLC (Brain and Acute Leukemia, Croplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCPNSOSLSSGPLTOKONGLWTTEAKRDAKRMSAREVAISVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKBVTINVTDSIQQMDRSRRITKNCVN 180
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                           Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GVLEDGPSSNGVLRPAPPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                     DB 7; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brain and Acute Leukemia, Cytoplasmic alternate protein #5.
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myelogenous leukemia; gene expression; BAALC;
                                                                                                                                                                                                                                                                                                                                     80.5%; Score 617.5; DB 7 67.2%; Pred. No. 1.6e-59; tive 10; Mismatches 14
                                                                                                              Disclosure; SEQ ID NO 19; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM46963 standard; protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanner SM, De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Matches 121; Conservative
WPI; 2003-441564/41.
N-PSDB; ADM46953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-441564/41.
                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADM46955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                       Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003040347-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM46963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM46963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

cancer

```
The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or The methods, kits and probes are useful for characterizing acute or formic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
BAALC transcripts in cells obtained from the patient.
                                                                                                 Disclosure; SEQ ID NO 21; 78pp; English.
```

Sequence 149 AA;

```
61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                               9
                                                                                                       82
                                                      53
                                                                 -----GVLEDGPSSNGVLRPAAPGGIANPEKKMNCGT
                             Gaps
                             35;
                                                  1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-
Score 473.5; DB 7; Length 149;
Pred. No. 9.8e-44;
2; Mismatches 12; Indels 35
                                                                                                                                                                      OCPNPQSLSSGPLTQKQNGLQTTE 144
                                                                                                                                                      QCPNSQSLSSGPLTQKQNGLWTTE
 61.7%;
             Best Local Similarity 66.0
Matches 95, Conservative
                                                                                                    54
Query Match
                                                                                                                                                      98
                                                                        엄
                                                                                                                           g
                                                 ò
                                                                                                                                                    ò
                                                                                                                                                                              a
                                                                                                 ð
```

ADQ81902 standard; protein; 92 ADQ81902; RESULT 11 ADQ81902

Æ

09-SEP-2004 (first entry) Human dioxygenase 10.12 

Human; enzyme; dioxygenase 10.12; malignant tumour; inflammation; immunological disease; haemopathy; HIV infection.

Homo sapiens

CN1344798-A.

17-APR-2002

29-SEP-2000; 2000CN-00125495

29-SEP-2000; 2000CN-00125495

(SHAN-) SHANGHAI BIODOOR GENE DEV CO LID.

Mao Y,

2002-509506/55.

N-PSDB; ADQ81901

New polypeptide human dioxygenase 10.12 and polynucleotides encoding this polypeptide, useful for treating various diseases, such as malignant tumors, inflammations, immunological diseases, hemopathy and HIV infection.

Claim 1; SEQ ID NO 2; 33pp; Chinese

The present invention discloses a new kind of polypeptide, human

```
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; screening whether an agent alters the expression of PAIGB mRNA; screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related
                                                                                                                                                                                                                                               58 DGPSSNGVLRPAAPGGIANPEKKANCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRM 117
dioxygenase 10.12, polymucleotides encoding this polypeptide, a DNA recombination process to produce the polypeptide and antagonist against the polypeptide. The present invention also discolases the method of applying the polypeptide in treating various diseases, such as malignant tumours, inflammations, immunological diseases, heamopathy and HIV infection. The present sequence is the human dioxygenase 10.12.
                                                                                                                                                                                                                                                                         ||| :
| DGPETGN-----APGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRM 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone density modulation;
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel PTH responsive gene (PAIGB) fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTH responsive gene; PAIGB; bone-forming; bone; bone density modul: transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing
                                                                                                                                                                        Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murrills RJ;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse PTH responsive gene protein exon 2 splice variant.
                                                                                                                                                                        DB 5;
                                                                                                                                                                                                              10;
                                                                                                                                                                      43.7%; Score 335.5; DB 9 72.7%; Pred. No. 8.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babij P,
                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                          118 SAREVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                            related disorders, e.g., osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; SEQ ID NO 10; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robinson JA, Stojanovic-Susulic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO48481 standard; protein; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-2003; 2003WO-US035655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-420299/39.
                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADO48480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004044152-A2.
                                                                                                                                   Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMHP ) WYETH
                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO48481;
                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  murine
                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO48481
   8888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                         셤
```

chastoaters; evaluating the eliteacy of a treatment of a bous treatment of a subject identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA; an animal model of or the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone discorders; identifying an agent of for treating bone related disorders; identifying whether an agent of the transfer of the part efficacy of a treatment of a bone related

Sequence 54 AA;

Gaps 54 54 1 MGCGGSRADAIEPRYYESWTRETESTWLIYTDSDALPSAAATDSGBEAGGLHAG 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG ö 38.3%; Score 294; DB 8; Length 54; 100.0%; Pred. No. 1.5e-24; tive 0; Mismatches 0; Indels 54; Conservative Similarity Query Match Best Local g à

ö

RESULT 13

ADM46962 standard; protein; 73 AA ADM46962

ADM46962;

03-JUN-2004 (first entry)

3rain and Acute Leukemia, Cytoplasmic alternate protein #4.

myelogenous leukemia; prostate cancer; Brain and Acute Leukemia; acute myelogenous leukemia; gene expression; BAALC; Cytoplasmic; exon. 

Homo sapiens

Location/Qualifiers Misc-difference 41

/note= "encoded by GCS"

WO2003040347-A2.

15-MAY-2003

12-NOV-2002; 2002WO-US036375.

09-NOV-2001; 2001US-0348210P.

(OHIS ) UNIV OHIO STATE RES FOUND.

De La Chapell A; Tanner SM,

WPI; 2003-441564/41. N-PSDB; ADM46954.

Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.

Disclosure; SEQ ID NO 20; 78pp; English

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
     The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAMLC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAMLC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acute myelogenous leukemia; gene expression; BAALC;
chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or prostate cancer
                                                                                                                                                                                                                                                                                                                 1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLED 58
                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGGLHSGCLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Characterizing acute or chronic myelogenous leukemia, or prostate canc
in a patient comprises assaying for the overexpression of one or more
BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brain and Acute Leukemia, Cytoplasmic alternate protein #2.
                                                                                                                                                                                                                                        Score 288; DB 7; Length 73; Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 18; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM46960 standard; protein; 54 AA.
                                                                                                                                                                                                                                    37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-2001; 2001US-0348210P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanner SM, De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OHIS ) UNIV OHIO STATE RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                               53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-441564/41.
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic; exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADM46952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003040347-A2
                                                                                                                                                                                                      Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2004
                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
ADM46960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                        g
```

The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; cobtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody.

CC a paign polypeptide; a composition for regulating bone-forming activity in a agent that alters the expression of PAIGB mRNA; creening whether an agent alters the expression of PAIGB mRNA; creening magnets for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the effectiveness in altering expression of the nucleic acid fragment; a transgenic animal comprising the bNN; an animal model for the study of bone density modulation comprising a first group of animals; studying bone mass determinants; studying whether an agent for the transgenic animal and second group of animals; studying an effect of PAIGB on bone disorders; identifying whether an agent for treating bone mass determinants; studying the mass etterminants; studying whether an agent for treating dome mass determinants; studying an effect of PAIGB on bone disorders; identifying whether an agent for two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain nucleic acid fragment encoding a PAIGB polypeptide, useful in paring a composition for diagnosing, treating or preventing bone preparing a composition for diagnosing related disorders, e.g., osteoporosis. Claim 9; SEQ ID NO 6; 169pp; English. Ź ADO48477 standard; protein; 54 36.2%; 10-NOV-2003; 2003WO-US035655. 12-NOV-2002; 2002US-0425532P. (first entry) Conservative WPI; 2004-420299/39. Similarity N-PSDB; ADO48476 WO2004044152-A2 Sequence 54 AA; (AMHP ) WYETH sapiens 12-AUG-2004 51; 27-MAY-2004 AD048477; Query Match Local Homo Matches RESULT 15 ADO48477

ADO48477

ADO504 ADO504 ADO505 ADO Š g ਨੇ

ö PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; human. Gaps 54 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG . 0 Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ; Length 54; Indels Human PTH responsive gene protein exon 2 splice variant. Score 278; DB 7; I Pred. No. 8.8e-23; 1; Mismatches 2;

ö all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention. Gaps 54 54 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG .. Length 54; 36.2%; Score 270; DB 8; Length 54 94.4%; Pred. No. 8.8e-23; ive 1; Mismatches 2; Indels Search completed: November 17, 2004, 15:22:21 Job time : 101 secs 51; Conservative Similarity Sequence 54 AA; Query Match Local Matches 888888888888 ઠે g

```
Query Match 11.0%; Score 84; DB 4; Length 726; Best Local Similarity 35.1%; Pred. No. 0.96; Matches 27; Conservative 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-328-352-8115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5198347-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8115, Ap Sequence 2, Appli Sequence 176, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli Sequence 473, Appli S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469, App
469, App
469, App
469, App
496, App
494, App
475, App
475, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16753, A
Sequence 23204, A
                                                                                                                                                 November 17, 2004, 15:02:57; Search time 24.3333 Seconds (without alignments) 395.183 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 494,
Sequence 494,
Sequence 475,
Sequence 475,
                                                                                                                                                                                                                                                                                                     1 MGCGGSRADAIEPRYYESWT......VTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4
Sequence 4
Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: /@gn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /@gn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /@gn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /@gn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /@gn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /@gn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-408-647A-2

US-09-408-647A-2

US-09-071-035-176

US-08-374-077C-2

US-08-374-077C-2

US-08-559-87A-2

US-09-121-964-1

US-09-121-964-1

US-09-121-964-1

US-09-14-259-10

US-09-413-8268-473

US-09-413-8268-473

US-09-644-759-473

US-09-590-751A-473

US-09-590-751A-473

US-09-590-751A-469

US-09-620-4058-469

US-09-620-4058-469

US-09-640-258A-469

US-09-640-258A-469

US-09-640-258A-469

US-09-640-258A-469

US-09-640-258A-469

US-09-640-258A-469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-620-405B-494
US-09-834-759-494
US-09-620-405B-475
US-09-604-287A-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                               478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                   US-10-705-716A-2
767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5
79.5
78.5
78.5
78.5
78.5
                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number
                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
```

```
Sequence 8115, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
PAPLICANT: GARY INVENTION: BLEEON et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8115
LENGTH: 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,
                                                                                                                                                    16, Appl
2, Appli
16745, A
19245, A
43092, A
7653, Ap
394, App
21991, A
27673, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18465, A
32740, A
17765, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGV-LRPAAPGGIANPEKKMNC-GTQCP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                            Sequence 2
Sequence 2
Sequence 2
                                                                                                          Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                           Sequence
Sequence
Sequence
                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MILLEY, LOUIS H.; ADAMS, JOHN H.; KASLOW, PALENT NO. 5198347

APPLICANT: MILLEY, LOUIS H.; ADAMS, JOHN H.; KASLOW, JOANIC C.; FANG, XIANGDOUG

TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND; PLASMODIUM KNOWLESI DUFFY RECEPTOR

NUMBER OF SEQUENCES: 27

CURRENT APPLICATION DATA;

ACHING DATE: 20-JUL-1990
             US-09-590-751A-475
US-09-620-405B-493
US-09-814-759-493
US-09-252-991A-18465
US-09-252-991A-1765
US-09-252-991A-1765
US-09-252-991A-1765
US-09-252-991A-16789
US-09-252-991A-16789
US-09-252-991A-16789
US-09-270-767-43092
US-09-252-991A-16783
US-10-140-002-394
US-09-252-991A-26962
US-09-252-991A-21991
US-09-252-991A-21991
US-08-252-991A-21991
US-08-352-991A-21991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 92.5; DB 33.0%; Pred. No. 0.11; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 NSQSLSS-GPLTQKQNGLWTTEAKRDAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT CORGANISM: Acinetobacter baumannii US-09-328-352-8115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.03
Matches 29; Conservative
1002
1002
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10095
10
```

4

Gaps

20;

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 176, Application US/09071035

Patent No. 6448043

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polymucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 TWANASAGSHTFKAVATDINNNAVTSSATVSVTVTASSNDTTPPSVPGGLASPSKTATTVN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 LVWSAATDNSGGSGVAGYDVYRNGSLVGSPSATQYTDGGLTASTAYTYTVRARDNAGNAS 278
2 GCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSA--AATDSG-----PEAGGLHAG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 TWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIANPEKKM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels 27; Gaps
                                           181 GFGAGREDVWEPDNDVNWGDEKE--WLAHRNSEALAGSNLAATEMGLIYVNPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
10.9%; Score 83.5; DB 3; Length 700;
Best Local Similarity 24.0%; Pred. No. 1;
Matches 31; Conservative 14; Mismatches 57; Indels 2
                                                                                                                                                                                                                                                                                                                     APPLICANT: Kobayashi, Donald
TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
TITLE OF INVENTION: Maltophila
FILE REFERENCE: Rut-Cook 98-0090
CURRENT APPLICATION NUMBER: US/09/408,647A
FILE SPELCATION NUMBER: 60/098,036
FILE SPELCATION NUMBER: 60/098,036
FILE SPELCE SPELCATION NUMBER: 60/098,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE ACCESSION NUMBER: Genbank No. 6399858 AF014950
DATABASE ENTRY DATE: 1997-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maltophilia
                                                                                                                                                                                                                                                     Sequence 2, Application US/09408647A Patent No. 6399858 GENERAL INFORMATION:
                                                                                                                         ----GPQASGDPRSAAP 244
                                                                                            55 VLEDGPSSNGVLRPAAP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Stenotrophomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SIGNAL
LOCATION: (1)...(41)
NAME/KEY: DOMAIN
LOCATION: (196)...(290)
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 AQSGSISVT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (330)...(483)
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AREVAISUT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NCG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-071-035-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 700
TYPE: PRT
                                                                                                                                                                                                            RESULT 3
US-09-408-647A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-408-647A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
Sequence 174, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polymucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 GLHAGVLEDGPSSNGVLRPAAPGGIANPEKKMN-CGTQCPN---SQSLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 STKEA-----ANNGSAEKQSPAKNANPDDQANQVLNQLANMFPGQGLPQAILTSQTNNF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CGG-----SRADAIEPRYYESW----TRETESTWLTYTDSDALPSAAAT-DSGPEAG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGGGKSTENTDSRSSAAESTTVESTKASATKESSSK-ATTKSSDAKPSGTTTADSKATAS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 WTTEAKRDAKRMSAREVAISVTENIRQMD-RSKRVT-------KNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.4%; Score 79.5; DB 4; Length 286;
Best Local Similarity 26.6%; Pred. No. 0.83;
Matches 47; Conservative 16; Mismatches 73; Indels 4.
Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                MSDOS version 6.2
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
                   COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 anino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
                                                                                                                                                        FILING DATE:
CLASSIFICATION:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-071-035-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-071-035-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-895-590-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ጵ
                                                                                                                                                                                              ð
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 GLHAGVLEDGPSSNGVLRPAAPGGIANPEKKMN-CGTQCPN---SQSLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 STKEA-----ANNGSAEKQSPAKNANPDDQANQVLNQLANMFPGQGLPQAILTSQTNNF 132
                                                                                                                                                                                                                                                                                                                                                                                                    3 CGG-----SRADAIEPRYYESW----TRETESTWLTYTDSDALPSAAAT-DSGPEAG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                           20 CGGGKSTENTDSRSSAAESTTVESTKASATKESSSK-ATTKSSDAKPSGTTTADSKATAS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 LTAATTSQADQNNFRVLYYAEKEAIPVNDARVNQLTPISSFEKKTYGSDAEAKNAVN 189
                                                                                                                                                                                                                                                                                                                                                      73; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                        ch 10.4%; Score 79.5; DB 4; Length 305; 1 Similarity 26.6%; Pred. No. 0.91; 47; Conservative 16; Mismatches 73; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08374077C
Patent No. 6027912
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
TITLE OF INVENTION: Calcium Channel Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NATA: US/08/374,077C FILING DATE: 19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 WITEAKRDAKRMSAREVAISVTENIROMD-RSKRVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: AND ATTORNEY/AGENT INFORMATION:
NAME: MCGOWAIN, MAICOLM M.
REGISTRATION NUMBER: 39,300
REGISTRATION NUMBER: 022650-264
REGISTRATION NUMBER: 36,373
REFERENCE/POCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFRAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 2516 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                     LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-374-077C-2
                                                                                                                                                                                                                        ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-09-071-035-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
```

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CGGSRADAIEPRY--YESWIRETESTWLIYIDSDALPSAAAIDSGPEAGGLHAGVLEDGP 60
                                                                                  3 CGGSRADAIEPRY--YESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                         QSLSSGPL-TOKONGLWTTEAKRDAKRMSAREVAISVTENIROMDRSKRVTKNC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 78.5; DB 3; Length 2516; 22.4%; Pred. No. 25; ive 21; Mismatches 61; Indels 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hall, Linda M.
APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dibald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
DB 3; Length 2516;
                                                                                                                            207 CGGGGISAPPPRLTPEEAWQLQPQ------NSVTSAGSTNSSFSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: BURNS, DOANE, SWECKER & MATHIS,
                                         21; Mismatches
10.2%; Score 78.5; 1
22.4%; Pred. No. 25;
                                                                                                                                                                          61 SSNGVLRPAAPGGIANPEKKMNC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   022650-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/374,888
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SSNGVLRPAAPGGIANPEKKMNC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              US-08-895-590-2; Sequence 2, Application US/08895590; Patent No. 6207410; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2516 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.4%
Matches 39; Conservative
                                           39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
```

q

셤 à

```
2 STTIEVTOKOLHDLLEIFEKKPFDAGSCEKGSLEEDITNRCEFLFKKDYTLIELDNSNGV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 GGLHAGVLEDGPSSNGVLRPAAPGGI-----ANPEKKMNCGTQCPNSQSLSSGP---L 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- PSSNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 TOKONGLWTTEAKR-----DAKRMSAREVAISVTEN----IROMDRSKRVT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LRPAAPGGIANPE-----KKMNCGTQCPNSQSLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LSPRYPGRIFIPEYEHGHMTSTITPNNTNLGTQATNHASPQSG---KNGNGL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 104, Application US/09220528A; Patent No. 6284540
; GENERAL INFORMATION: APPLICANT: Milbrandt, Jeffrey D. APPLICANT: Baloh, Robert H. ; TITLE OF INVENTION: Arremin, A No. 6284540el Neurotrophic Factor; FILE REFERENCE: 6029-7998
                                                                                                                APPLICANT: Natori, Shunji
TITLE OF INVENTION: NOVEL ENZYME CATALYZING DEPHOSPHORYLATION
FILE REFERENCE: 32290-144753
CURRENT APPLICATION NUMBER: US/09/121,964
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.2%; Score 78; DB 3; Length 724;
Best Local Similarity 28.6%; Pred. No. 4.7;
Matches 32; Conservative 6; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 78; DB 4; Length 885; 29.6%; Pred. No. 6.3; tive 16; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09914259; Patent No. 6495336; GENERAL INFORMATION:
APPLICANT: MAKOWSKI, Lee; APPLICANT: Hyman, Paul; APPLICANT: Williams, Mark; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES; FILE REFERENCE: 8471-010-999; CURRENT APPLICATION NUMBER: US/09/914,259; CURRENT FILING DATE: 2000-11-21; NUMBER OF SEQ ID NOS: 180; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 STWLTYTDSDALPSAAATDSGP-EAGGLHAGVLEDG-
                                                 ; Sequence 1, Application US/09121964; Patent No. 6124447; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Sarcophaga peregrina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-220-528-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-914-259-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-914-259-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    882
                                                                                                                                                                                                                                                                                                                                                                  US-09-121-964-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
250 DDNSSY--SAVGGDSSSSNSCNCDITGDNSTLHGLGVGDVCSFIADCDDNSEDDDGDPNN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 DDNSSY--SAVGGDSSSSNSCNCDITGDNSTLHGLGVGDVCSFIADCDDNSEDDDGDPNN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CGGSRADAIEPRY--YESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
                                                                        OSLSSGPL-TOKONGLWTTEAKRDAKRMSAREVAISVTENIROMDRSKRVTKNC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSLSSGPL-TOKONGLWTTEAKRDAKRMSAREVAISVTENIROMDRSKRVTKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                           Zheng, wei
Zheng, wei
Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
Calcium Channel Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 2516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,879A
FILLING DATE: 31-Mar-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/111,865
FILLING DATE: 10-MAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 022650-264
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.2%; Score 78.5; 1
Best Local Similarity 22.4%; Pred. No. 25;
Matches 39; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-539-879A-2
                                                                                                                                                                                                  Sequence 2, Application US/09539879A
Patent No. 6436627
GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
Ren, Dejian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2516 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SSNGVLRPAAPGGIANPEKKMNC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VA
COUNTRY: USA
                                                                                                                                                                           US-09-539-879A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
```

g ð 임 ò

Matches

g

ò

```
78 RADEILPSESKQKDYEESSWDSESICETVSQKDVCLPKAAHQKEIDKIN----GKLEESP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 DNDGFLKAPCRMKVSIPTKALELMDMQTFKABPPEKPSAFEPAIBMQKSVPNKALELKNE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 RADEILPSESKOKDYEESSWDSESLCETVSOKDVCLPKAAHOKEIDKIN----GKLEESP 133
                                             APPLICANT: Jiang, Yuqui
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Mitchan, Jennifer L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121-470C4
CURRENT PELLING DATE: 1999-11-03
CURRENT FILING DATE: 1999-11-03
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NCGTOCPNS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 RADAIEP----RYYESWTRETESTWLTYTDSD-ALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NCGTQCPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 RADAIEP-----RYYESWTRETESTWLTYTDSD-ALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 473, Application US/09604287A
; Sequence 473, Application US/09604287A
; Referr No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Hallocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.47007
; CURRENT FILIAG DATE: 2000-06-22
; WUNBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; IND NO 473
; INDICATION: 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 OSLSSG---PLTQKQNGL----WTTEAKRDAKRMSAREVAISVTENIRQMDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.1%; Score 77.5; DE
Best Local Similarity 21.5%; Pred. No. 2.7;
Matches 37; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.1%; Score 77.5; DE 21.5%; Pred. No. 2.7; tive 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SSNGVLRPAAPGGIANPEKKM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SSNGVLRPAAPGGIANPEKKM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.59
Watches 37, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-09-433-826B-473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-604-287A-473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::| |:
134 DNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NCGTQCPNS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AYWAPGPCD----RPRAPGPSASP-------AADPRATKRSPSWTSTA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 GVLEDGPSSNGVLRPAAPGGIANPEKKANCGTQCPNSQSLSSGPLTQKQNGLWTTEA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 RADAIEP----RYYESWTRETESTWLTYTDSD-ALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GSRADAIEPR----YYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER FILE REFERENCE: 210121.47008
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DAIRS: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FREESE FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| : | | : ::||: CTLRADQMFPSESKQKKVEENSWDSESLRET--VSQKDVCVPKATHQKEMDK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 QSLSSG---PLTQKQNGL----WTTEAKRDAKRMSAREVAISVTENIRQMDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                             10.1%; Score 77.5; DB 3; Length 215; 26.5%; Pred. No. 0.93; tive 12; Mismatches 41; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.1%; Score 77.5; DB 4; Length 445;
Best Local Similarity 21.5%; Pred. No. 2.7;
Matches 37; Conservative 28; Mismatches 58; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Indels
APPLICATION NUMBER: US/09/220,528A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SSNGVLRPAAPGGIANPEKKM------
                  CURRENT FILING DATE: 1999-12-24
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER PILING DATE: 1998-12-22
EARLIER PILING DATE: 1998-11-12
EARLIER PILING DATE: 1998-11-12
EARLIER PILING DATE: 1998-11-12
EARLIER PILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
SCOFTWARE: PARENTIN Ver. 2.0
SEQ ID NO 104
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 473, Application US/09620405B Patent No. 6528054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 473, Application US/09433826B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Conservative
                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-220-528-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-620-405B-473
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-620-405B-473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-433-826B-473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 473
LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
```

7;

9

90

7;

Gaps

g

à

ò 셤 ò

```
134 DNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMOKSVPNKALELKNE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 RADAIEP-----RYYESWTRETESTWLTYTDSD-ALPSAAATDSGPEAGGLHAGVLEDGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NCGIQCPNS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Indels 49; Gaps
                                                                                                                               RESULT 15
US-09-834-759-473
i Sequence 473. Application US/09834759
j Patent No. 6680197
j GENERAL INFORMATION:
j APPLICANT: Dillon, Davin C.
j APPLICANT: Dillon, Davin C.
j APPLICANT: Mitcham, Jennifer L.
j APPLICANT: Mitcham, Jennifer L.
j APPLICANT: Harlocker, Susan L.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j APPLICANT: Hepler, William T.
j TILLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
j TILLE OF INVENTION: UNMERS: US/09/834,759
j CURRENT FILING DATE: 2001-04-13
j SEQ ID NO 473
j SEQ ID NO 473
j TIPE: PRT
j CORGANISM: Homo sapiens
US-09-834-759-473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 OSLSSG---PLTQKQNGL----WTTEAKRDAKRMSAREVAISVTENIRQMDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 OSLSSG---PLTQKQNGL----WTTEAKRDAKRMSAREVAISVTENIRQMDR 135
                              Query Match 10.1%; Score 77.5; DB 4; Length 445; Best Local Similarity 21.5%; Pred. No. 2.7; Matches 37; Conservative 28; Mismatches 58; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 17, 2004, 15:30:02 Job time: 25.3333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SSNGVLRPAAPGGIANPEKKM-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
   à
                                                      D
```

```
November 17, 2004, 15:22:38 ; Search time 81.3333 Seconds (without alignments) 631.334 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWT........VTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*

1: \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{VSOT} \) \( \text{FMP PUB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOG} \) \( \text{NEW PUB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{NEW PUB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{NEW PUB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{NEW PUB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{PuBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{PuBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{PuBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{PuBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{PuBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USOT} \) \( \text{PuBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USIDD.PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USIDD.PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USIDD.PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USIDD.PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USIDD.PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USIDD.PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \text{USIDD.PUBCOMB.pep:*} : \) \( \text{cgn2} \) \( \text{fptodata} / 2 \) \( \text{Pubpaa} / \t
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1570615 segs, 354127592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-705-716A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITAMADITEC

					SUMMAKIES		
		oks.					
Result		Query	Query				
No.	Score	Match	Length	DB	ID	Description	
-	645	84.1	145	14	IIS-10-293-239-17	1.4	
,			! :		17 (57 57 57 57	1/1	
7	045	84.1	145	74	US-10-177-390-30	Seguence 30, Appl	
٣	617.5	80.5	180	14	US-10-293-239-19	19	
4	473.5	61.7	149	14	US-10-293-239-21	, [	
Ŋ	288	37.5	73	14	US-10-293-239-20	Semience 20 and	
9	278	36.2	54	14	US-10-293-238	2 0	
7	272	4	α		TIG-10-201-20	2 0	
. (		) !	3	7	77-667-667-01-60	sednence zz, Appl	
00	140	18.3	25	14	US-10-293-239-37	Sequence 37. Appl	
σ	99	12.9	18	14	US-10-293-239-35		
-	94	13.3		7	110 00 100 000 000 000	מלקע זכר במונאה המ	
2	r :	77.3	*	9	US-TO-/9/-/0T-80	Seguence 48905, A	
11	93	12.1	394	17	US-10-425-115-236244	Segmence 236244.	
12	85.5	11.1	264	17	US-10-425-115-275422		
	u				100110 101 101 011		
7	0	77.7	# 7	C	US-10-425-114-6558B	Sequence 65588, A	

Sequence 137075, Sequence 45268, A Sequence 60, Appl Sequence 112, App	Sequence 227399, Sequence 144983, Sequence 140197, Sequence 180225,	Sequence 1945, Ap Sequence 14107, A Sequence 43318, A Sequence 188141,	Sequence 176, App Sequence 176, App Sequence 174, App Sequence 174, App Sequence 552, App	Sequence 552, App Sequence 552, App Sequence 553, App Sequence 553, App Sequence 553, App Sequence 553, App	
US-10-437 US-10-282 US-09-801-					US-10-437-963-13251 US-10-424-599-242710 US-10-424-599-19556 US-10-451-467A-554 US-10-087-192-1317 US-10-080-608A-10 US-10-370-685-99 US-10-437-963-180217 US-09-220-920-104
15	16	14 11 10 10 10	14 6 11 13 13 13 13 13 13 13 13 13 13 13 13	14 14 14 14 17	155 115 114 114 114 116
450 718 1433 1433	609 1491 1597	600 320 508	286 305 305 661	661 661 1013 1013 1013	262 355 455 661 832 885 1479 215
111.0	10.8	10.6	1011	100 100 4.00 100 100 100 3	100000000000000000000000000000000000000
8 8 8 8 5 2 4 8 8 1	82.5 82.5 82.5	81.5 80.5 80.5		79.5 79.5 79.5 79.5	78.5 78 78 78 78 78 78
14 15 17	18 20 21 21	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	22 28 29 30	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Ს Ს Ს Ს Ქ Ქ Ქ Ქ Ქ Ს Ს Ს Ს Ქ Ქ Ქ Ქ Ქ Ქ Ს Გ Ს Ს Ს Ს Ს Ქ Ს Ს

## ALIGNMENTS

```
Sequence 17, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia FILE REFERCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%; Score 645; DB 14; Length 145; 83.4%; Pred. No. 8e-57; Live 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EVIINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.49
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 17
LENGTH: 145
TYPE: PRT
US-10-293-239-17
                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-293-239-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
Sequence 20, Application US/10293239

Sequence 20, Application US/10293239

Sequence 20, Application WS/10293239

Publication No. US20030119043A1

GENERAL INFORMATION:

APPLICANT: Tanner, Stephan

APPLICANT: del la Chapelle, Albert

TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia

FILE REFERENCE: 22727/04101

CURRENT ELLING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: US 60/348,210

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

SEQ ID NO 20
                                                                                                                                                                                                                                       APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US, 10/293, 239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
54 ------GVLEDGPSSNGVLRPAAPGGIANPEKKWNCGT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 37.5%; Score 288; DB 14; Length 73; 1 Similarity 91.4%; Pred. No. 3e-21; 53; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 473.5; DB 14; Length
Pred. No. 1.5e-39;
2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 OCPNPÓSLSSGPLTOKONGLOTTE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OCPNSOSLSSGPLTOKONGLWTTE
                                                                                                                                                           ; Sequence 21, Application US/10293239; Publication No. US20030119043A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.0
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-293-239-20
                                                                                                                                      US-10-293-239-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-293-239-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 149
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 QCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTBAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
                                                                                                                                                                                                                                               of Eucaryotic Cells with Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GVLEDGPSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.5%; Score 617.5; DB 14; Length 180; Best Local Similarity 67.2%; Pred. No. 6.2e-54; Matches 121; Conservative 10; Mismatches 14; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match

84.1%; Score 645; DB 14; Length 145;
Best Local Similarity 83.4%; Pred. No. 8e-57;
Matches 121; Conservative 10; Mismatches 14; Indels
                                                                                                        Sequence 30, Application US/10177390
| Publication No. US20030143743A1
| GENERAL INFORMATION:
| APPLICANT: SCHIEK, Gerold
| APPLICANT: N.V. Antwerps Innovatiecentrum
| TITLE OF INVENTION: Improved Transfection of Eucaryotic Cell
| TITLE OF INVENTION: Delynuclectides by Electroporation
| FILE REFERENCE: 021505wo/JH/ml
| CURRENT FILING DATE: 2002-06-20
| NUMBER OF SEQ ID NOS: 34
| SOFTHARE: Patentin Ver. 2.1
| SEQ ID NO 30
| LENGTH: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EVIINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-293-239-19; Sequence 19, Application US/10293239; Publication No. US20030119043A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-293-239-19
                                                                   RESULT 2
US-10-177-390-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-177-390-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 19
```

à 임 ò 원 ò 원

ij

ö

엄 à g ò

à

ო

```
1 RADAIEPRYYESWTRETESTWLTYT 25
                                                                                                                                                                                                                                                                                7 RADALEPRYYESWTRETESTWLTYT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48905, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-293-239-35
Sequence 35, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 DAIBPRYYESWTRETEST 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Sorghum bicolor
                                                                                                 ; ORGANISM: Homo sapiens
US-10-293-239-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-767-701-48905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-293-239-35
                                                                            TYPE: PRT
                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
Matches 1
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/10293239

| Sequence 22, Application US/10293239
| Publication No. US20030119043A1
| Sequence 22, Application No. US20030119043A1
| Publication No. US20030119043A1
| GENERAL INFORMATION:
| APPLICANT: Tanner, Stephan
| TILLE OF INVENTION: BALLC expression as a diagnostic marker for acute leukemia |
| TILLE OF INVENTION: BALLC expression as a diagnostic marker for acute leukemia |
| TILLE OF INVENTION: BALLC expression as a diagnostic marker for acute leukemia |
| TILLE OF INVENTION NUMBER: US/10/293,239 |
| CURRENT APPLICATION NUMBER: US/10/293,239 |
| PRIOR FILING DATE: 2001-11-09 |
| NUMBER OF SEQ ID NOS: 39 |
| SOFTWARE: PatentIn version 3.1 |
| SEQ ID NO 22 |
| LENGTH: 80 |
                                                                                    APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT PILING DATE: 2002-11-12
PRIOR RIPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVERTION: BAALC expression as a diagnostic marker for acute leukemia FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR PUBLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 278; DB 14; Length 54;
Pred. No. 2.1e-20;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.5%; Score 272; DB 14; Length 80; 94.3%; Pred. No. 1.4e-19; tive 1; Mismatches 2; Indels
                  Sequence 18, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.44
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.5
Best Local Similarity 94.3
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-293-239-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-293-239-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
APPLICANT: Tanner, Stephan
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
CURRENT APPLICATION HUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 48905
LENGTH: 147
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 LPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQS---
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                   ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
ch 18.3%; Score 140; DB 14; Length 25; 1 Similarity 100.0%; Pred. No. 6.2e-07; 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
12.3%; Score 94; DB 16; Length 147;
Best Local Similarity 27.5%; Pred. No. 0.24;
Matches 30; Conservative 17; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.9%; Score 99; DB 14; Length 18; 100.0%; Pred. No. 0.0055; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: LIB3476-020-P1-K1-A12.pep
US-10-767-701-48905
```

```
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                           셤
                                                                                         ਨੇ
                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 275422, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: 203. Younger US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 275422
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: In COMPANDED.

APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 LSSGPLTQKQNG-----LWTTE----AKRDAKRMSA------ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 PSAAATDSGPEAGGLHAGVLEDGP-SSNGVLRPAAPGGIANPEKKMNCGTQCPN---SQS 92
29 LPAALAPEDAGEAEGADNGGAHRGPHRG----QAERAGAGARDGALHCGPPCPHSDSCIG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
12.1%; Score 93; DB 17; Length 394;
Best Local Similarity 27.0%; Pred. No. 1.1;
Matches 40; Conservative 21; Mismatches 43; Indels 44; Gaps
                                                                                                                                                                                   --LSSGPLTQKQ-NGLWTTEAKRDAKRMSAREVAISVTENIRQMDRSKR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 85.5; DB 17; Length 264; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_147036C.1.pep
US-10-425-115-236244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: MRT4577_182776C.1.pep
US-10-425-115-275422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 -- REVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 RRLQLDFSKSQLVEKLRRLKRKYRNCVS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 236244, Application US/10425115 Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-115-236244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-425-115-275422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                      à
```

```
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 137075
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 65588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 DSDDAPAAAAHDDQPAAVVAAGGLGGGNSSSG-LPPAAAGAATAEAEPSLSLGLPLP 205
                                                                                                                            137 DSDDAPAAAAHDDQPAAVVAAGGLGGGNSSSG-LPPAAAGAATAEAEPSLSLSLGLPLP 195
                                                        32 DSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGI---ANPEKKMNCGTQCP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 DSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGI----ANPEKKONCGTOCP 88
21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                              196 AAEPAEAAADDESRNSQGQAS-PLIEEGEG--NAQLIAVVRRWVREEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 AAEPAEAADDESRNSQGQAS-PLLEEGEG--NAQLLAVVRRMVREEV 250
                                                                                                                                                                                                   -----NSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.1%; Score 85.5; DB 15; Length 2 Best Local Similarity 32.4%; Pred. No. 3.8; Matches 35; Conservative 10; Mismatches 42; Indels
42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Clone ID: LIB4863-011-F12_FLI.pep
US-10-425-114-65588
35; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 137075, Application US/10437963
| Publication No. US2004012334341
| GENERAL INFORMATION |
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Cao, Yongwei |
| APPLICANT: Boukharov, Andrey A. |
| APPLICANT: Boukharov, Andrey A. |
| APPLICANT: Boukharov, Andrey A. |
| APPLICANT: Boukharov, Andrey A. |
| APPLICANT: Boukharov, Andrey A. |
| APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 65588, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
```

```
셤
                                                                                                                                   ò
                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                   60 -----DGPSQDG------GSEAAKKKKK-----SKSKKKKGPLQQTDPPSIPIDELF 101
                                                                                                                                                                             4 GGSRADAI------EPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLH 52
                                                                                                                                                                                                                                3 GGS-ADAVTKEMEALLVGONPNAVSGETCETSSKEGKVADSNGSHSSPPEDDDDEAQG-- 59
                                                                                                                                                                                                                                                                                                                                                                                   101 ------KONGLW--TTEAKRDAKRM----SAREVALSVTENIRQMDRS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-20-20
                                                                                                                                                                                                                                                                                                                                                                                                                      102 PSGDFPEGEIQQYKDDNLWRTTSEEKRELERLQKPMYNAVRRAAEVHRQVRKHMRS 157
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 45568
LENGTH: 718
                                                                                                                                                                                                                                                                                   53 AGVLEDGPSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQ-----
                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.0%; Score 84; DB 15; Length 718; Best Local Similarity 35.1%; Pred. No. 18; Matches 27; Conservative 8; Mismatches 22; Indels
                                                                                  Length 450;
                                                                                                                                53; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38593C.1.pep
US-10-437-963-137075
                                                                        11.1%; Score 85; DB 16; 25.6%; Pred. No. 8; ative 14; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45268, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-010-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Acinetobacter baumannii
US-10-282-122A-45268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                             45; Conservative
                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-282-122A-45268
                                                                                                                                Matches
                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
```

22; Indels 20; Gaps

```
-- 223
2 GCGGSRADAIEPRYYESWIRETESTWLTYIDSDALPSA--AATDSG-----PEAGGLHAG 54
                           Search completed: November 17, 2004, 15:48:52 Job time : 93.3333 secs
                                                                                                               || ::| ||||
224 ----GPQASGDPRSAAP 236
                                                                                      55 VLEDGPSSNGVLRPAAP
```

us-10-705-716a-2.rpr

```
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
```

OM protein - protein search, using sw model

November 17, 2004, 15:00:21 ; Search time 19.6667 Seconds (without alignments) 709.395 Million cell updates/sec Run on:

US-10-705-716A-2 Perfect score:

1 MGCGGSRADAIEPRYYESWT...........VTENIRQMDRSKRVTKNCIN 145 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		de				
Result	·	Query				
. No.	Score	Match	Length	8	QI	Description
н	92.5	12.1	571	7	T43456	hypothetical prote
7	92.5	12.1	778	7	A35970	erythrocyte-bindin
m	88	11.5	365	٦	GNVSSC	genome polyprotein
4	83	10.8	1433	7	S54587	CAT8 protein - vea
Ŋ	81	10.6	269	7	T37073	
9	81	10.6	196	7	S66852	
7	79.5	10.4	2559	ď	T09144	ㅁ
89	78.5	10.2	1199	N	A40670	OU.
σ	78	10.2	882	N	T09225	w.
10	78	10.2	3488		T34418	ical pr
11	76.5		600		668690	conserved hypothet
12	92	9.	645		S19156	serotonin receptor
13	16		839		E84824	O
14		9.8	499		S22571	×
15	75.5		1063		T03743	bifocal protein -
16	75.5	9.8	1122	~	T47424	hypothetical prote
17	75		368	Н	TVMSML	transforming prote
18	75	9.8	521	7	151693	XPolycomb - Africa
19	74.5	9.7	601	ď	AH0784	Ţ
20	74.5	9.7	4957	N	T03455	ALR protein - huma
21	74.5		5262	~	T03454	1
22	74		260	~	B38594	1
23	74		742	7	T38001	Ø
24	74		832	~	T31878	
25	74		962	ď	T00262	
56	73.5	•	876	Н	A57988	н
27	73.5	•	096	N	T37916	probable heterochr
28	73.5		1575	~	S6844B	~~
59	73	9.5	403	ď	H98327	enantiomer-selecti

glutamyl-tRNA amid	nypochetical prote enamelin matrix pr	cytochrome-related	transcription fact	prepilin (imported	probable solute-bi	inulinase (EC 3.2.	cell division prot	intrinsic factor-B	microtubule-associ	hypothetical prote	DNA-directed DNA p	DNA polymerase del	3-dehydroguinate s	8-amino-7-oxononan
AE2955	T37193	C75521	151172	AG1028	T35053	JE0301	AF0611	T08618	T13564	T31565	JC5757	T18222	T50113	AB3048
0,0	v 6	7	~	~	ď	7	N	~	N	~	Н	~	7	7
453	1274	251	284	435	503	216	1343	3623	5327	108	1038	1038	1573	381
o o	, o	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	4.6	4.6	4.6	9.4	9.3
73	73	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72	72	72	72	71.5
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
hypothetical protein DKFZp434L061.1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 1-dan-2000 #text_change 09-Jul-2004 C;Accession: T43456 F;Alein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, December 1999 A;Accession: T43456 A;Accession: T43456 A;Status: preliminary A;Accession: T43456 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-571 <AAA A;Acsidues: 1-571 <AAA A;Accession: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:AL133647 A;Cross-references: UNIPROT:075175; EMBL:Al133647 A;Cross-references: UNIPROT:075175; EMBL:Al133647 A;Cross-references: UNIPROT:075175; EMBL:Al133647 A;Cross-references: UNIPROT:075175; EMBL:Al133647 A;Cross-references: UNIPROT:075175; EMBL:Al133647 A;Cross-references: UNIPROT:075175; EMBL:Al133647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---AGVLEDGPSSNGVLRPAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 --GGIANPEKKMNCGTQCPNSQSLS----SGPLT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 12.1%; Score 92.5; DB Local Similarity 31.9%; Pred. No. 0.95; nes 30; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 TDSDALPSAAATDSGPEAGGLH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

111 TDSEVSQSPAKNGSKPVHSNQHPQSPAVPPTYPSGPPPAASALSTTPGNNGVPAPAAPPS 170

3;

#### RESULT 2

C;Species: Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Rate: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change 09-Jul-2004
C;Ratesion: A35970
R;Adams, J.H.; Hudson, D.E.; Torii, M.; Ward, G.E.; Wellems, T.E.; Aikawa, M.; Miller, L.
Cell 63, 141-153, 1990
A;Title: The duffy receptor family of plasmodium knowlesi is located within the micronem A;Reference number: A35970
A;Reference number: A35970
A;Reference preliminary
A;Molecule type: DNA
A;Residues: Ly78 <ADA>
A;Residues: L-778 <ADA>
A;Cross-references: UNIPROT:P22545; GB:M68518; GB:M37513; NID:g160273; PID:g160274
C;Reywords: transmembrane protein

Gaps 3; Length 778; 44; Indels Query Match 12.1%; Score 92.5; DB 2; Best Local Similarity 33.0%; Pred. No. 1.4; Matches 29; Conservative 12; Mismatches 44;

3;

N

à

```
A;Residues: 1-302/A,,304-767,'A',769-998,1003-1007,'S',1009-1015,'Q',1017-1018,'P',1026
A;Cross-references: EMBL:X94215; NID:g1122900; PIDN:CAA63906.1; PID:e214033; PID:g112296
A;Experimental source: strain ENY.WA-1A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SCJ30.06c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37073
S;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.Reference number: Z21621
A;Reference number: Z21621
A;Accession: T37073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q9S1Y3, EMBL:AL109973; PIDN:CAB53301.1; GSPDB:GN00070; SCOE A,Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-967 <ARI>
A;Cross-references: UNIPROT:Q08294; EMBL:Z74897; NID:g1420063; PID:e251930; PID:g142006
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S66852

S66852

NyAlternate names: hypothetical protein 00419; protein AOF1001

NyAlternate names: hypothetical protein 00419; protein AOF1001

C;Species: Saccharowyces cerevisiae
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004

C;Accession: 866852; 866854; 870380

R;Arino, J; Casamayor, A.; Gamo, F.J; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, submitted to the Protein Sequence Database, July 1996

A;Rcference number: 866814

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           927 LPPATTTSLKPLFGSQSKNSLENRQRTPNVKR-----ENPEHEYLYGNDSNNNNSEA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 IEPRYYESWT-----RETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 LPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      980 GHSPMTUTTNGNKRLKYEKDAKR-NAKDGGISKGENAHNFQNDTKKNMS 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G--PLIQKONGLWTTEAKRDAKRMSAREVAISVTENIR--OMDRSKRVT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 83; DB 2; Length 1433; 29.4%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81; DB 2; Length 269;
Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Indels
                                                                                                                                                                                                                                                                                                                                       C;Keywords: transmembrane protein
F;65-102/Domain: GAL4 zinc binuclear cluster homology <(
F;456-472/Domain: transmembrane #status predicted <TMl>
F;78-754/Domain: transmembrane #status predicted <TMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GGGVVTTGAGGGIV-PGEACRCGRAAHAPTNASMRS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SSNGVLRPAAPGGIANPEKKMNCG--TQCPNSQSLSS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-269 <SAN>
                                                                                                                                                                                                     A,Gene: SGD:CAT8; MSP8
A,Cross-references: SGD:S0004893; MIPS:YMR280c
A,Map position: 13R
C,Superfamily: GAL4 zinc binuclear cluster homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Gene: SCOEDB:SCJ30.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1433 <PEA>
A;Cross-references: UNIPROT:P39113; EMBL:Z49704; NID:g825540; PIDN:CAA89778.1; PID:g8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P25242, GB:D00948, NID:g222123; PIDN:BAA00796.1; PID:g222124 C;Superfamily: tobacco etch virus genome polyprotein C;Keywords: coat protein; inclusion protein F;1-52/Product: nuclear inclusion protein (fragment) #status predicted <IPB>F;53-365/Product: coat protein #status predicted <COA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: PH0207
R;Frenkel, M.J.; Jilka, J.M.; McKern, N.M.; Strike, P.M.; Clark Jr., J.M.; Shukla, D.D.
R;Frenkel, M.J.; Jilka, J.M.; McKern, N.M.; Strike, P.M.; Clark Jr., J.M.; Shukla, D.D.
J. Gen., Virol. 72, 237-242, 1991
A;Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins
A;Reference number: PH0207, MUID:91132116; PMID:1993866
A;Accession: PH0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 OGGAOPPATGAAAOPPTTO--GSOLPOGGATGGGGAOTGAGGTGSVTGGORDKDVDAGTT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 NGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREV 122
                                                                                                                                        352 TVSSDVPSVGGKDSGPSTSASHALAGENGEVHNGTDTEPKEDGEKADPQKDIEVKGKQDT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GIKEEEIE-KYFKQFAKDLPGYLEDYND-EVFHQAGTVDAGAQGGGGNAGTQPPATGAAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATB protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: MSP8 protein; protein YM8021.06c; protein YMR280c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul.1995 #sequence revision 01-Sep-1995 #text_change 16-Aug-2004
C;Accession: S54587; S48234; S61595; S49498
                                                                                                                                                                                                                                                                                                                                                                                                                                       genome polyprotein - sugarcane mosaic virus (strain SC) (fragment)
N;Contains: carboxyl end of nuclear inclusion protein b; coat protein
C;Species: sugarcane mosaic virus, SCMV
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVL--EDGPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-746,1L',748-1433 <GRZ>
A;Residues: 1-746,1L',748-1433 <GRZ>
A;Cross-references: EMBL:X78344; NID:9559523; PIDN:CAA55139.1; PID:9559524
R;Boles, E.; Hettmann, C.; Zimmermann, F.K.
R;Boles, E.; Hettmann, C.; Zimmermann, F.K.
A;Reference number: S61594
A;Accession: S61595
                                                                              TDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGV-LRPAAPGGIANPEKKMNC-GTQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.5%; Score 88; DB 1; Length 365; Best Local Similarity 21.6%; Pred. No. 1.5; Matches 30; Conservative 24; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Experimental source: strain AB972
R, Grzesitza, D.
submitted to the EMBL Data Library, March 1994
A, Reference number: $48234
A, Accession: $48234
                                                                                                                                                                                                                                                                             DDRSQGSLGPHTDERATIGETHMEKDTE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54582
A;Accession: S54587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AISVTENIROMDRSKRVTK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 GKITVPKLKAMSKKMRLPK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: genomic RNA
A; Residues: 1-365 < FRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                           셤
                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                             셤
```

```
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A40670
R;Hallberg, E.; Wozniak, R.W.; Blobel, G.
A;Ritlle: 01. 122, 513-521, 1993
A;Ritle: wan integral membrane protein of the pore membrane domain of the nuclear envelop.
A;Reference number: A40670; MUID: 93328754; PMID: 8335683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P52591; GB:Z21513; NID:g396746; PIDN:CAA79725.1; PID:g396747.
F;803-807,845-849,956-960,1010-1014,1047-1051,1076-1080/Region: pentapeptide motif (X-F-)
                                                           A,Description: mediates actin rearrangements required for cell shape changes during gast: C;Superfamily: rat Munc13-3 protein; protein kinase C zinc-binding repeat homology C;Keywords: embryo; GTP exchange; signal transduction F;1151-1200/Domain: protein kinase C zinc-binding repeat homology <KZN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A kinase anchor protein AKAP-KL isoform 1 - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Jate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C.Accession: T09225; T09226; T09227 T09226; T09227 R.Spong, F.; Feldmesser, M.; Casadevall, A.; Rubin, C.S. Biol. Chem. 273, 6533-6541, 1998 A;Title: Molecular characterization of a cDNA that encodes six isoforms of a novel murint A;Reference number: 216620; MUID:98165844; PMID:9497389
                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422
                                                                                                                                                                                                                                                                                                                                                                                                                                  799 GSSPDNMHPRHPDRITKTISGSW-EIVEKDGESSPPGIPPPPYLSSSHMTVLEDPNENNR 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 ERPAKKTR--EEEPCHÓSSSSAPLVTDKESPGEKVTDPATGKÓQSLWTSPPTPGSSGQRK 480
                                                                                                                                                                                                                                                                                                                                                                       GSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-885 <DON>
A;Residues: UNIPROT:054931; EMBL:AF033274; NID:92852696; PID:92852697
A;Cross-references: UNIPROT:054931; EMBL:AF033274; NID:92852696; PID:92852697
A;Note: binds the regulatory subunits (RII) of protein kinase AII isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|:::|||::|||::|||
363 SRTSSVSSLTSTCTGGIPSSSRNAITSSYSSTRGVSQLWKRSGPTSSPFSSPASSRSQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 TRETESTWILYTDSDALPSA---AATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIA-
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                         DB 2; Length 2559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 10.2%; Score 78.5; DB 2; Length 1199; I Similarity 25.2%; Pred. No. 43; 39; Conservative 19; Mismatches 56; Indels 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TOKONGLWTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 VLRPAAPG-GIANPEKKMANCGTQCPNSQSLSSGPL-----TQKQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               858 GAAAAGPGVFIESHOFTPMAGASSPIPISLHSNHMHAAQSNDTQKE 903
                                                                                                                                                                                                                                                                                                        Indels
orchestrates cell shape changes during gastrulation
                                                                                                                                                                                                                                                                                                 :95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 RDAKRMSAR-----EVAISVTENIRQMDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 RKIQLLPSRRGDQLTLPPPPELGYSITAEDLDMER 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T09225
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                               Query Match
10.4%; Score 79.5; D
Best Local Similarity 28.3%; Pred. No. 84;
Matches 30; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nuclear envelope protein POM 121 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 -NPEKKMNCGTQCPNSQSLSSGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1199 <HAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T09226
                                                                                                                                                                                                                                                                                                                                                                       Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
Matches 3
                                  C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A40670
                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   슝
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                    핑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
kholecule type: DNA
A;Residues: 55-164, STSITSGSSSATESGSSVSGSTSATESGSSASGSS',166-186,'V',188-286;745-773;781
A;Cross-references: EMBL:X89715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable guanine nucleotide exchange factor RhoGEF2 - fruit fly (Drosophila melanogaster N;Alternate names: Shar pei/DRhoGEF2 C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Daces: Drosophila melanogaster C;Daces: Il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: T00144; T09223 R;Haecker, U.; Perrimon, N. submitted to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                  щ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Analysis of the DNA sequence of a 15,500 bp fragment near the left telomere of and two new open reading frames.

A;Reference number: $70379; MUID:96405919; PMID:8810044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-676,'L',678-837,'L',839-889,'S',891-1243,'D',1245-1358,'E',1360-1368,'R',1
A;Cross.references: EMBL:AF032870; NID:g2760367; PIDN:AAC38820.1; PID:g2760368
                                                                                                                                                                                 A;Cross-references: EMBL:274897; NID:g1420063; PID:e251930; PID:g1420064; MIPS:YOL155c A;Experimental Bource: strain $288C
A;Experimental Bource: M.J.; Casamayor, A.; Aldea, M.; Casas, C.; Ario, J.; Herrero, E submitted to the EMBL Data Library, July 1955
A;Description: Analysis of the DNA sequence of a 15500 bp fragment of the left arm of c A;Reference number: S67324
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S67325
A;Molecule type: DNA
A;Residues: 1-164, STSITSGSSSATESGSSSVSGSTSATESGSSASGSS',166-186,'V',188-967 <GAM>
A;Residues: 1-164, STSITSGSSSATESGSSVSGSTSATESGSSASGSS',166-186,'V',188-967 <GAM>
A;Cross-references: EMBL:X89715; NID:g1177620; PID:e190152; PID:g1177622
R;Gamo, F.J.; Lafuente, M.J.; Casamayor, A.; Arino, J.; Aldea, M.; Casas, C.; Herrero, Yeast 12, 709-714, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-2559 cHAB.
A;Residues: 1-2559 cHAB.
A;Cross-references: UMLPROT:044113; EMBL:AF031930; NID:g2687355; PID:g2687356
B;Barrett, K; Leptin, M.; Settleman, J.
Cell 91, 905-915, 1997
A;Title: The Rho GTPase and a putative RhoGEF mediate a signaling pathway for the A;Reference number: Z16618; MUID:98088790; PMID:9428514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 SSASESSITQSGTASGSSASSTSGSVTQSGSSVSGSSAS-----SAPGISSSIPQS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 GIANPEKKANCGTOCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREVAISVTEN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 ESWITRITESIWLTYIDSDALPSAAAIDSGPEAGG----LHAGVLEDGPSSNGVLRPAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ESGSSASGSSSATESGSSVSGSSSATESGSSSSATESGSASSVPSSSGSVTESGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.6%; Score 81; DB 2; Length 967; 24.8%; Pred. No. 20; rative 23; Mismatches 55; Indels
                    submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: FlyBase:FBgn0023172
A;Map position: 2; 53F1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: SGD:S0005515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                       A; Reference number: S66854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: 216586
A;Accession: T09144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                     A; Residues: 1-967 <GAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S70380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 15L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T09223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: YOL155c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: rhoGEF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
A;Cross-references: UNIPROT:034330; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13792 A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signification receptor 2B - fruit fly (Drosophila melanogaster)
NyAlternate names: 5-hydroxytryptamine receptor 2B (5-HTR2B)
NyAlternate names: 5-hydroxytryptamine receptor 2B (5-HTR2B)
C;Species: Drosophila melanogaster
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S19156; S18154
E;Saudou, F.; Boschert, U.; Amlaiky, N.; Plassat, J.L.; Hen, R.
E;Saudou, F.; Boschert, U.; Amlaiky, N.; Plassat, J.L.; Hen, R.
E;Saudou, F.; Boschert, U.; Amlaiky, N.; Plassat, J.L.; Hen, R.
E;Saudou, F.; Boschert, U.; Amlaiky, N.; Plassat, J.L.; Hen, R.
E;Saudou, F.; Boschert, U.; Amlaiky, N.; Plassat, J.L.; Hen, R.
E;Saccession: S19155; MUD:92155185; PMID:1310937
A;Title: A family of Drosophila serotonin receptors with distinct intracellular signall
A;Residues: 1-645 <8AU>
A;Residues: 1-645 <8AU>
A;Residues: 1-645 <8AU>
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Gene: FlyBase: FBgn0004572
C;Genetics:
A;Gene: FlyBase: FBgn0004572
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM2>
F;124-145/Domain: transmembrane #status predicted <TM3>
F;284-305/Domain: transmembrane #status predicted <TM4>
F;284-305/Domain: transmembrane #status predicted <TM5>
F;584-587/Domain: transmembrane #status predicted <TM6>
F;597-619/Domain: transmembrane #status predicted <TM6}
F;597-619/Domain: transmembrane #status predicted <TM6}
F;597-619/Domain: transmembrane #status predicted <TM6}
F;597-619/Domain: transmembrane #status predicted <TM6}
F;597-619/Domain: transmembrane #status predicted <TM6}
F;597-619/Domain: transmembrane #status predicted <TM6}
F;597-619/Domain: transmembrane #status predicted <TM6}
F;597-619/Domain: transmembrane #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 DAISAAIEESYQKDMVNGDAYSRSRWTY----AIGSVAVAVVGTKG----AGAINKADA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AGKVINKASQAGKKIKDVKIPDLLPYNPKYKLALADNVPYNVVDSQNLKNELLTNAKKIP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 TYTDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGG----IANPEKKMNCG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 DAIEPRYYESWTRE-----TESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 SNGVLRPAAPGGIA-----NPEKKMNCGTQCP----NSQSLSSGPLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 -----QKQNGLWTTEAKRDAKRMSAREVAISVTENIRQMDRSKRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 DGTRKPFTGQKKSPPWLNKEKYD-----AYEIEGKVKAKGKVKDVSRRV 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%; Score 76; DB 2; Length 645; 31.0%; Pred. No. 36; tive 12; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 76.5; D
ilarity 23.1%; Pred. No. 30;
Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Conservative
Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-600 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: yobL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69899
R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2818 PVKILVPGSEMPASK----TEKK----TDAAKSESEQKSAEEIVAEKQVDQSQASES 2866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 GSIHS----DKPPT--ILRPATVGGTLEDGGTQAAKEQKAPCVSE---SQSAGAGPANAA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-3488 <FUL>
A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3
A;Experimental source: strain Bristol N2; clone F12F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GGLHAGVLEDGPSSNGVLRPAAPGGI-----ANPEKKWNCGTQCPNSQSLSSGP---L 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypotherical protein F12F3.3 - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 (C,Accession: T3418 B. Wohldmann, P. Submitted to the EMBL Data Library, July 1998 A,Description: The sequence of C. elegans cosmid F12F3. A,Reference number: Z21521 A.Accession: T34418
                         A/Cross-references: EMBI-AF033275; NID:g2852698; PID:g2852699
A/ROGES binds the regulatory subunits (RII) of protein kinase AII isoforms
A/Accession: T09227
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; brodylated from GB/EMBL/DDBJ
A/Status: preliminary; brodylated from GB/EMBL/DDBJ
A/ROGES in 1789, pGGHTG' < DOJ3
A/Cross-references: EMBL.AF033276; NID:g2852700; PID:g2852701
A/ROGES: binds the regulatory subunits (RII) of protein kinase AII isoforms
C/Genetics:
A/Genetics:
A/Genetics: AKAP-KL
C/Keywords: alternative splicing; kidney; lung; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ESTWL--TYTDSDALPSAAATDSGP-----EAGGLHAGVLEDGPSSNGVLRPAAPGGIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VSSPSEETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 PEKKMANCGIQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREVAI-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 TQKQNGLWTTEAKR-----DAKRMSAREVAISVTEN----IRQMDRSKRVT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%; Score 78; DB 2; Leugua 24.3%; Pred. No. 1.6e+02; Migmatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 5
A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein yobL - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2772 DSDWLEIANTDRNKFKDRSLTESGEYVYQVTATGIHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.2%; Score 78; DB 2
Best Local Similarity 29.6%; Pred. No. 34;
Matches 34; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || : ::|:| |
2867 TTEAVEE-KKTKKVVK 2881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTENIROMDRSKRVTK 141
       A;Residues: 1-848,862-885 <DO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: CESP: F12F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

7;

Gabs

4.

	Db 77 PSQGNSPQEESQLTWTGF Qy 73 GIANPEKKMNGTQCPNGF
RESULT 13 E84824 E84824 C:Patetical protein At2g40040 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004	Db 119 GLKDPEGTLDFS.  Qy 132 QMDRSKRVTKNCI 144
Cyncoension: E84824 R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84824 A;Actession: E84824	RESULT 15 T03743 T03743 Diffical protein - fruit fly (Drc C; Species: Drosophila melanogast C; Date: 24-Mar-1999 #sequence_reC; Accession: T03743
N:AAB95289.1; GSPDB:GN	K. Hanti, S.M.; Yang, X.Y.; Chla, Mol. Cell. Biol. 17, 5521-5529, A;Title: The Drosophila bifocal A;Reference number: 215048; MUID A;Accession: T03743 A;Status: preliminary; translate A;Molecule type: mRNA
Query Match 9.9%; Score 76; DB 2; Length 839; Best Local Similarity 23.8%; Pred. No. 49; Matches 40; Conservative 14; Mismatches 62; Indels 52; Gaps 6;	A; Cross-references: UNIPROT:016. C; Genetics: A; Cross-references: FlyBase:FBg
5 GSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAA	A;Note: bifocal  Query Match Best Local Similarity 20.7%;
42TDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIANPEKKM 81	Matches 39; Conservative  Qy 5 GSRADALEPRYYESWIR-
82 NCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDARRWSAREVAISVTEN 129	83.
	DD 143 NVIVIETENQESSELLINIE QY 73 GIANPEKKMNCGTQCPNS
822571 integrase-like protein FE65 - rat CiSpecies: Rattus norvegicus (Norway rat) CiDate: 31-Dec-1993 #sequence revision 02-Aug-1994 #Fext change 09-Jul-2004	203
n: S22571; S22572	248 CSKTKSIS
Tus Res. 15, 2403-3414, 1991 rat brain mRNA encoding a transcriptional activator homologous to the DNA bir e number: \$22571; WUID:92020215; PMID:1923810 n: \$22571 type: mRNA	Search completed: November 17, 2 Job time : 29.6667 secs
: 1-499 <duii>: 1-499 <duii>: 1-809 (NIPROT: 099MK3; EMBL: X60469; NID: 957559; PIDN: CAA42999.1; PID: 957560 nn: \$22572</duii></duii>	
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule 1999: DNA A;Residues: 31-318 <dui2> A;Cross-references: EMBL:X60468; NID:957561; PIDN:CAA42998.1; PID:91177617 A;Note: this sequence was submitted to the EMBL Data Library, July 1991</dui2>	
Query Match 9.8%; Score 75.5; DB 2; Length 499; Best Local Similarity 25.6%; Pred. No. 30; Matches 34; Conservative 17; Mismatches 59; Indels 23; Gaps 5;	

```
a, W.
, 1997
1. gene encodes a novel protein which colocalizes with actir
IID:97415628; PMID:9271427
                                                                                                                                                                                                                                                                                                                                                                                                                                                6125; EMBL: AF011791; NID: 92388667; PIDN: AAB69991.1; PID: 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                       NSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREVAISVTENIRQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPNHLK----TKCKPGQSVAEGKPSAKE------TIVDNSKS 247
IYIDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------DSGPEAGGLHAGVLEDGPSSNGVLRPAAPG 72
                                                                                                                                                                                                                                                                             revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R-----BTESTWLTYTDSDAL-------PSAAAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %; Score 75.5; DB 2; Length 1063;
%; Pred. No. 71;
23; Mismatches 59; Indels 67; Gaps
                                                                                                                                                                                                                                    rosophila melanogaster)
ster
                                                                                                                                                                                                                                                                                                                                                                                              ted from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004, 15:28:51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gn0014133
```

```
Q8VHV1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8wx83 homo sapien
Q9cys9 mus musculu
Q79013 rattus norv
Q8wb88 mus musculu
Q8wx90 homo sapien
Q8wxp6 homo sapien
Q8wx20 homo sapien
Q8wx22 homo sapien
Q8wx82 homo sapien
Q8wx82 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8tgel saccharomyc
Badd6576 saccharomyc
Q7uz29 rhodopirell
P50494 plasmodium
Q96a2 homo sapien
Q6u3f5 plasmodium
Aaq22950 plasmodium
Q8mtc2 leucophaea
                                                                                                                                                                                                                                                                                                                                                                                                                                             mus musculu
homo sapien
sus scrofa
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q801v5 brachydanio
Q6zmf homo sapien
Bad18729 homo sapien
P22545 plasmodium
Q8wao organiam
P25242 sugarcane m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sugarcane m
saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        076c74 saccharomyc
Bad06577 saccharom
                                                                                                                                                                                                                                                                                                                                                                                                                                    2920k5 rattus norv
                                                         November 17, 2004, 14:59:59; Search time 103.667 Seconds (without alignments) 804.784 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       1 MGCGGSRADAIEPRYYESWT......VTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8vhv1
Q9ha93
Q8wne9
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                           1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNO3_HUMAN
QBWOA_DLAKN
QBWOAO
POLG_SUMVS
Q76C74
BAD06577
Q3TGE1
Q7UZ29
PVDG_PLAKN
Q96SA2
QGUEFS
AGUPES
                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8WTP6
AAH35038
Q8WXS2
Q8WNE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q801V5
Q62MJ6
BAD18729
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q920K5
Q8VHV1
Q9HA93
Q8WXS3
Q8WXS1
Q9CYS9
Q790N3
Q8VBS8
                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                          UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
                                                                                                  US-10-705-716A-2
                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
1035
1035
1713
1713
1713
585
1070
534
155
155
                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.8
33.3
34.5
36.2
36.2
35.5
35.5
                                                                                                              Perfect score:
                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB s
Maximum DB s
                                                                                                                         Sequence:
                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                           Database
                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
```

030678 xanthomonas 08K0v4 mus musculu Q89ell bradyrhizob P89204 sugarcane m P39113 saccharomyc Q7sef2 neurospora Q6zq88 mus musculu Bac97980 mus muscu Q6bxp0 debaryomyce Q8krb5 streptomyce Q8krb5 streptomyce C13412 aspergillus Cas68196 aspergillus Q7xpbl Oryza sativ Q94ka7 phaseolus v	PRELIMINARY; PRT; 145 AA.  101 (TYEMBLYE1. 19, Created) 104 (TYEMBLYE1. 19, Last sequence update) 104 (TYEMBLYE1. 19, Last sequence update) 105 (TYEMBLYE1. 17, Last sequence update) 105 (TYEMBLYE1. 17, Last sequence update) 106 (TYEMBLYE1. 17, Last sequence update) 107 (TYEMBLYE1. 17, Last sequence update) 107 (TYEMBLYE1. 18) 107 (TYEMBLYE1. 18) 107 (TYEMBLYE1. 18) 107 (TYEMBLYE1. 18) 107 (TYEMBLYE1. 18) 107 (TYEMBLYE1. 19) 107 (TYEMBLYE1. 19) 107 (TYEMBLYEN	
030678 CN03 MOUSE Q89EL1 P89204 CAT8 YEAST Q7SEF2 AAC2 MOUSE BAC37980 Q6RXB5 AREA ASPNG CAA65196 Q7XPB1 Q94KA7 ALIGNMENTS	920K5  920K5  920K5  920K5  920K5  920K5  01-DEC-2001 (TERMBLrel. 19, Created) 01-DEC-2001 (TERMBLrel. 19, Last sequence update) 01-DEC-2001 (TERMBLrel. 19, Last sequence update) 01-DEC-2001 (TERMBLrel. 19, Last sequence update) 01-DEC-2004 (TERMBLrel. 27, Last annotation update) 01-DEC-2004 (TERMBLrel. 27, Last annotation update) Dem-A20-4 (BAALC isoform 1.6-8)  Name-dem-A20-4; Symonyms-Baalc; Name-dem-A20-4; Symonyms-Baalc; Rattus norvegicus (Rat).  Rattus norvegicus (Rat).  Rattus norvegicus (Rat).  Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Endamalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI TaxID=10116; [1]  SEQUENCE FROM N.A.  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ database (12) SEQUENCE FROM N.A.  STRAIN-Sprague-Dawley; MEDLINE-21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass MEDLINE-21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass MEDLINE-21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass MEDLINE-21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass MEDLINE-21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass MEDLINE-21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass Medlin Med. Sci. U.S.A. 98:13901-13966 (2001).  EMBL: ABAJOSO71: 1.  EMBL: AB731318; BABACC N.  100.00; Score 767; DB 2; Leng Metches 145; Conservative 0; Mismatches 0; Ind MATCHES 145; MATCHIRQMDRSKRUTKNCIN 145	PRT; 145 AA.
5 10.9 700 2 10.9 751 1 10.8 751 2 10.8 14.3 1 10.8 14.3 1 10.8 11.4 2 10.8 11.4 2 10.8 11.5 1 10.8 11.5 1 10.7 1 14.4 9 2 2 10.7 1 14.4 9 2 2 10.6 397 2	T.1  Q920K5  D1-DEC-2001 (TEEMBLRE1. 19, LEST as of D-DEC-2001 (TEEMBLRE1. 19, LEST as SECONDE-2004 (TEEMBLRE1. 17, LEST as SECONDE-2004 (TEEMBLRE1. 27, LEST as Dem-A20-4 (BAALC isoform 1-6-8).  Dem-A20-4 (BAALC isoform 1-6-8).  Rattus norvegicus (Rat).  Ratus (OCT-2001) to the EMBL/Ge (12)  SEQUENCE FROM N.A.  Submitted (OCT-2001) to the EMBL/Ge (12)  SEQUENCE FROM N.A.  SUBDINE-21574584; PubMed=11707601;  Tanner S.N., Austin J.L., Leone G.,  Arozek K., Sill H., Knuutila S., Korzek (Nat).  Arozek K., Sill H., Knuutila S., Korzek (Nat).  Arozek K., Sill H., Knuutila S., Korzek (Nat).  From, PRo6989; BAALC N. 1.  PRAM: AP371319; AALSOS17.1;  PRAM: PRO91318; BABNOSON.1;  PRAM: PRO91318; BAALC N. 1.  PRAM: PRO91318; BAALC N. 1.  PRAM: PRO91318; BAALC N. 1.  PRAM: PRO91318; BAALC N. 1.  PRAM: PRO91318; BAALC N. 1.  PRAM: PRO91318; BAALC N. 1.  PRAM: PRO91318; BAALC N. 1.  PRAM: PRO91318; BAALC N. 1.  1 MGCGGSRADAIEPRYYESWIRETEST  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SSNGVLRPAARGGIANPEKKANCCTO  61 SNGVLRPAARGGIANPEKKANCCTO	PRELIMINARY;
33 33 34 34 35 35 36 37 37 44 44 42 44 42 82 83 83 83 83 84 84 86 87 87 87 87 87 87 87 87 87 87 87 87 87	RESULT 1  0920K5  D	RESULT 2 Q8VHV1 ID Q8VHV1

us-10-705-716a-2.rup

and

Heinonen K.,

```
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-Cerebellum;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length DNN libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Cerabellum;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20530913; PubMed=11076861; Shibata X. Nagaoka S., Sasaki N., Carninci P., Shibata X., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata X., Itoh M., Alzawa Y., Nakamura S., Hazama M., Nishino H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa M., Obara E., Watahiki M., Poneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RISHIKA integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-007-2004 (TrEMBLrel. 28, Last annotation update)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
81-007-2004 (TrEMBLRel.)
8
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., Kolitz J.B., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Cerebellum; MEDLINE=2108566J; PubMed=11217851; RIKEN FANYOM CORSOCTIUM; "Punctional annotation of a full-length mouse cDNA collection."; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB=Cerebellum;
MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
Carlinol P., Hayashizaki Y.;
Migh-efficiency full-length cDNA cloning.";
Meth. Bnzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Cerebellum;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129S6/SvEvTac;
                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=10090;
                                                                                                                                                                                                         Name=Baalc;
```

```
RP 121

RP SEQUENCE FROM N.A.

RC TISSUE=Whole embryo;

RX Pubmed=14702039;

RA Ota T., Sauzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Atamatsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Atamatsu M., Kanda T., Iwayanagi T., Wadatsuma M., Shiratori A.,

RA Atahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Omura Y.,

RA Atahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Omura Y.,

RA Anioomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Ninomiya K., Ishidashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Anehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

RA Anehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Actsu M., Imose N.,

RA Musashino K., Yuuki H., Satoh N., Takami S., Terashima Y., Sano S.,

Yoshikawa Y., Momiyama H., Ichihara T., Shiohata N., Sano S.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fuliwara T.,

Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fuliwara T.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fuliwara T.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fuliwara T.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fuliwara T.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fuliwara T.,

RA Ayabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Kawabata A., Hikiji T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Senba T.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Senba T.,
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIBPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                    Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TERMBLE). 16, Last sequence update)
01-OCT-2004 (TERMBLE). 28, Last sequence update)
Hypotherical protein FLJ128, Last annotation update)
Hypotherical protein FLJ12015 (BAALC isoform 1-6-8) (Brain and acute leukemia, cytoplasmic) (BAALC 1-6-8).
       Koya S.,
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Obsato N., Okazaki Y., Saitoh H., Satai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takakahi A., Yanaka T., Tomaru A., Toya T., Yanuishi A., Muramatsu M., Hayashizaki Y., Submitted (Apr. 2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                        Length 145;
                                                                                                                                                                                                                                                                                                                                                   Score 746; DB 2; Lengtn 11-
Pred. No. 2.7e-59;
2; Indels
                                                                                                                                                                                                                                                    MGD; MGI:1928704; Baalc.
InterPro; IPR09728; BAALC.N.
Pfam; PF05999; BAALC.N; I.
SEQUENCE 145 AA: 15515 MW; 4972670A618C4D6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVAISVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                      EMBL; AF371320; AAL50516.1; -. EMBL; AK079337; BAC37611.1; -.
                                                                                                                                                                                                                                                                                                                                                                             97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 7...
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9HA93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09HA93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

145 AA.

PRT;

PRELIMINARY;

```
D8WNE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WXS3
                         ACCOCCOS DIT REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
Aptichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A'llalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
and mouse con Assertance and initial analysis of more than 15,000 full-length human
and mouse con Assertance and Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Matanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAATDSGPEACGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                           MEDLINE=21574584; PubMed=11707601;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozzek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 645; DB 2; Length 145;
; Pred. No. 3.3e-50;
10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AKO22077; BAB13960.1; -- EMBL; AF731319; AAL50515.1; -- EMBL; BC011517; AAH11517.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF363578; AAL50377.1; -.
InterPro; IPR009728; BAALC N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 145 AA; 15551 MW; CFB92BBR283DD92E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.1%;
                                                                                                                                                                                                                                                        Nat. Genet. 36:40-45(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.1%
Best Local Similarity 83.4%
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain
                                                                                                                                                                                                                   CDNAS
       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

ð

RESULT Q8WNE9

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21574584; PubMed=11707601;
MEDLINE-21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.,
"BAALC, the Numan member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
EMBL, R7363578, AALSO379:1;
InterPro; IPR06989; BAALC.N.
Pfam; PF06989; BAALC.N.
SEQUENCE 180 AA; 19224 MW; 380183E0F188F684 CRC64;
                                                                                                                                                                                                                                              Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIBPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                               Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                             lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL, AF371322; AALS0518.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.5%; Score 617.5; DB 2; Length 180; 67.2%; Pred. No. 1.3e-47; rive 10; Mismatches 14; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR009728; BALC.N.
Pfam; PF06989; BAALC.N; 1.
SEQUENCE 145 AA; 15401 MW; C75ED7D00EF82E26 CRC64;
                                          Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.7%; Score 634; DB 2;
82.8%; Pred. No. 3.2e-49;
iive 10; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EVTINVTESIRQVDRNQRITKKCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 EVAISVTENIROMDRSKRVTKNCIN 145
    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                             MEDLINE=21574584; PubMed=11707601;
                     (TrEMBLrel. 20, (TrEMBLrel. 26,
    20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 121; Conservative
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                           BAALC isoform 1-6-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAALC 1-5-6-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002
01-MAR-2002
                                                                                   Name=BAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WXS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O8WXS3
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
SO DER LA PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE PRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAFGGIPNPEKKTNCET 120
                                                                                                                                                                                                61 KIKAPTDSVSDEGLFSASKMAPLAVFSHĠMLEDĠLPSNĠVPRSTAPGGIPNPEKKTNĊET 120
                                                                                                                                                                            QCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 ------GVLEDGPSSNGVLRPAAPGGIANPEKKMNCGT
                                        MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
                                                                                        ----GVLEDGPSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heinonen K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810457D07 product:brain and acute leukemia,
cytoplesmic, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDALPSAAAIDSGPEAGGLHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 473.5; DB 2; Length 149;
Pred. No. 9e-35;
2; Mismatches 12; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Hein Mrozek K., Sill H., Knuutila S., Kolitz J.B., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
BAALC, the human member of a novel mammalian neuroectoderm glineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR009728; BAALC N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 149 AA; I5577 MW; DB26C19969B91F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCPNSOSLSSGPLTQKQNGLWTTE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCPNPOSLSSGPLTOKONGLOTTE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF363578; AAL50381.1; -. Genew; HGNC:14333; BAALC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 66.0
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BAALC 1-5-6-7-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                            54
                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9CYS9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9CYS9
                                                                                                                                                                                                                                                                                                                                    Q8WXS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9CYS9
                                                                                                                                                                                                                                                                                                                  O8WXS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                            ð
                                                                                                                                     g
                                                                                                                                                                                   à
                                                                                                                                                                                                                         d
```

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.

Mus musculus (Mouse)

NCBI\_TaxID=10090;

```
Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,

Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukwa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Salito H., Salito R., Ohno M.,

Okazaki Y., Okido T., Owa C., Salito H., Salito R., Sakia R.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagawi M., Tagawa A., Takahashi F., Tanaka T.,

A Pojima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,

Muramateu M., Hayashizaki Y.,

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO13358, BAB28608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AGVLEDGPSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIR=CS7BL/Gd, TISSUE=Whole body;
MEDLINE=C97BL/Gd, TISSUE=Whole body;
MEDLINE=C97BL/Gd, TISSUE=Whole body;
MEDLINE=C97BL/Gd, TISSUE=Whole body;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 SGVLEDGLSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUB=Whole body;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kaisunai T., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kaisunai T., Tashiro H., Itoh M., Yamamoto R., Matemura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matemura S., Izawa M., Ohara E., Watahiki M., Voneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Inoue Y., Kira A., Hayashizaki Y.; Rishika integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.8%; Score 459; DB 2; Length 12: 94.6%; Pred. No. 1.6e-33; wiematches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13391 MW; 33DFCB5F8CFAA0AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 DAKRMSAREVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM CONSORTIUM,
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Whole body;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/61; TISSUE=Whole body;
MEDLINE-21085660; PubMed=11217851;
                                                                                                        Carninci P., Hayashizaki Y.,
"High-efficiency full-length c
Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1928704; Baalc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

54 54

Q790N3;

0790N3

```
1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=21574584; PubMed=11707601;

MEDLINE=21574584; PubMed=11707601;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,

Mrozek K., Sill H., Knutila S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene
proc. is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-1574584; PubMed=11707601; Rush L.J., Plass C., Heinonen J Manner S.M., Augutin J.L., Leone G., Rush L.J., Plass C., Heinonen J Mrozek K., Sill H., Knutila S., Kolitz J.B., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).

EMBL; AFS36781 AAL50380.1; -.

InterPro: IPR009728; BAALC.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                             1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 288; DB 2; Length 73
Pred. No. 1.9e-18;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7871 MW; 98DBC2E6E6EF524A CRC64;
                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2002 (TYEMBLrel. 20, Last sequence upd 05-JUL-2004 (TYEMBLrel. 27, Last annotation u BAALC isoform 1-8 (BAALC protein) (BAALC 1-8)
                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 AA
                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.4%;
                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            BAALC 1-4-5-6-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissum=Brain;
                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004
                                                                                                                                                                                                                                                                                                       01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                           Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8WTP6;
                                                                                                                                                                                                                                                QBWXS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8WTP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                     QBWXS
                                                                                                                                                                                                                                                      ODT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DOT TO DO
                                          à
                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-12956/SvEvTac;
MEDLINE-21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
Mrozek K., Sill H., Knuulla S., Kolltz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. US.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K. Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEBRYYESWTRETBSTWLTYTDSDALPSAATDSGPEAGGLHAG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
BMB1, AR71325; AALSO521.1; -
InterPro. IPR009728; BAALC.N.
Ffam; PP06989; BAALC.N, I.
SEQUENCE 54 AA; 5667 MW; FEB8COEBFBCDB829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.3%; Score 294; DB 2; Length 54; 100.0%; Pred. No. 3.8e-19; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1928704; Baalc.
InterPro; IPR009728; BAALC N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 54 AA; 5667 MW; PERBCOEBFBCDB829 CRC64;
                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.3%; Score 294; DB 2; I
100.0%; Pred. No. 3.8e-19;
iive 0; Mismatches 0;
Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 AA
                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley;
MEDLINE=21574584; PubMed=11707601;
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                         BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] =
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                        Name=Baalc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Baalc;
                                 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

Q8VBS8;

**08VBS8** 

RESULT 9 Q8VBS8

g ò

Matches

. 0

Gaps

.; 0

```
SEQUENCE FROM N.A.
                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lineage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8WNE8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBWNE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WXS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8WXS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
Q8WXS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O8WNE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID ACCOOR OD THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ THE READ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
         à
                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEDLINE=2238825; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toobhlyuki S., Carninci P., Prange C., A Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H., Britard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Almwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Norley R.A., Chimwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Norley R.M., Marra M.A., Touchman J.W., Genen E.D., Dickson M.C., Scherztion and initial analysis of more than 15,000 full-length human M. Mannan M. Mannan M. Mannan M. Mannan M. Mannan M. Mannan M.M. Scheneration and initial analysis of more than 15,000 full-length human M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Mannan M.M. Manna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 278; DB 2; Length 54; Pred. No. 1.1e-17; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF371323; AAL50519.1; -.
EMBL; BC035038; AAH35038.1; -.
EMBL; AF363578; AAL50378.1; -.
InterPro; IPR009728; BAALC_N.
Pfam; PF06989; BAALC_N; SEGUENCE 54 AA; 5663 MW; PEF0B4EABED9B829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 94.4%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAALC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH35038
AAH35038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH35038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                  d
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=215/4584; PubMed=11707601;
MEDLINE=215/4584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
Englich in M.A., Bloomfield C.D., de la Chapelle A.;
Inneage, is implicated in novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Ara63878; AL50382.1;
EMBL; AR363878; AL50382.1;
Enterpro; IPRO09728; BAALC_N.
Fram; PP06989; BAALC_N;
Engure B.O. A.; 8573 MW; 70BE9991C3245E2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=21574584; PubMed=11707601;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,

Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

BAALC, the human member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                       1 MGCGGSRADAIBPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                     ;
                                                                                                            Score 278; DB 2; Length 54;
Pred. No. 1.1e-17;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 272; DB 2; Length 80 Pred. No. 5.8e-17; 1 Mismatches 2; Indels
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                      FEF0B4EABED9B829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                         36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20,
20,
                                                                      54 AA; 5663 MW;
                                                                                                                                                   94.48;
                                                 EMBL; BC035038; AAH35038.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                        51, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                   Best Local Similarity
Matches 51, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
```

;

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                          0;
                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
SI:2C215113.3 (Novel protein similar to human brain and acute leukemia, cytoplasmic (BAALC) (Fragment).
                                                                                                    Query Match

34.8%; Score 267; DB 2; Length 54;
Best Local Similarity 92.6%; Pred. No. 1e-16;
Matches 50; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.0%; Score 161; DB 2; Length 32; 90.6%; Pred. No. 1.9e-07; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sehra H.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AL807244; CADB7801.1; -.
Inter'ed. IRR009728; BAALC_N.
Pfam; PF06989; BAALC_N.
NON TER 32
SEQUENCE 32 AA; 3663 MW; 916A5445D263B7F7 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL; AF371326; AAL50522.1; -
Interpror IPR009728; BAALC.N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 54 AA; 5681 MW; 6538C3DABED9B825 CRC64;
                                                                                                                                                                                                                                                                                              32 AA.
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.61
Matches 29; Conservative
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     à
```

à

Search completed: November 17, 2004, 15:27:45 Job time : 113.667 secs

Н

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

November 17, 2004, 14:59:59; Search time 103.667 Seconds (without alignments) 804.784 Million cell updates/sec

US-10-705-716A-4
778
1 MGCGGSRADAIEPRYYESWT.....VTDSIQQMDRSRRITKNCVN 145

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

•• Database

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	neines omod 89a490	рошоц	Sus	mus	ratt		พนธ	homo	Q8wtp6 homo sapien	Aah35038 homo gapi	Q8wxs2 homo sapien	Sug	ratt		brac		_	09m291 arabidopsis					Q8gan3 arthrobacte	Q8le41 arabidopsis			34 su		Aas05144 mycobacte	O828t2 streptomyce	
SUMMAKIES	ID	O9HA93	Q8WXS3	Q8WNE9	QBVHV1	Q920K5	Q8WXS1	Q9CYS9	Q8WXS0	Q8WTP6	AAH35038	Q8WXS2	Q8WNE8	Q790N3	Q8VBS8	Q801V5	Q72HQ2	AAS81776	S24C ARATH	055597	Q6C2R4	Q6FKP2	P5PA_RAT	Q8GAN3	Q8LE41	09ZX85	Q767L8	BAD08434	Q73W33	AAS05144	Q828T2	000
	DB	101	~	~	7	~	7	~	7	7	(1	~	7	N	~	N	~	N	-	N	N	7	Н	~	N	N	~	N	N	7	N	•
	Length	145	180	145	145	145	149	123	73	54	54	80	54	54	54	32	306	306	1097	1625	291	717	1001	221	222	249	2042	2042	189	189	670	
*	Query Match	100.0	96.5	85.3	83.4	82.9	73.2	49.0	39.7	38.4	38.4	37.7	36.2	35.7	35.7	20.7	12.5	12.5	12.3	12.1	12.0	11.9			٠	٠	11.8	11.8	11.7	11.7	11.7	, ,
	Score	778	750.5	664	649		569.5	381	309	299	299	293	282	278	278	161	97.5	97.5	95.5		'n	92.5	92.5	σ	٠	91.5	91.5	91.5	91	91	91	0
	Result No.	Н	7	е	4	Ŋ	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	

# ALIGNMENTS

```
MEDLINE=21574584; PubMed=11707601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WNE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
Q8WNE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID DIT AND SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                           Attaches and a second and a second and a second and a second and a second a second and a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a second a seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PSNGVPRSTAPGGI PNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWIRETESTWLIYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 778; DB 2; Length 145;
; Pred. No. 3.6e-55;
0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK022077; BAB13960.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFB92BBE283DD92E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVIINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF371319; AAL50515.1; -.
EMBL; BC011517; AAH11517.1; -.
EMBL; AF365578; AAL50377.1; -.
InterPro; 1PR009728; BAALC.N.
Pfam; PF06899; BAALC.N; 1.
SEQUENCE 145 AA; 15551 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAALC 1-5-6-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                  IISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08WXS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WXS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8WXS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

[1] SEQUENCE FROM N.A.

NCBI\_TaxID=9606;

Name=BAALC;

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=2154584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
Mrozek K., Sill H., Knutila S., Kolitz J.E., Archer K.J.,
Caligluri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
EMBL, AF371322; AAL50518.1; -.
InterPro, IRRO09728; BAALC N.
EFGUENCE 145 AA; 15401 MW; C75ED7D00EF82E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSNAAPDSGPEAGGLQAGVLEDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWIRETESTWLTYIDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGCGGSRADAIBPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                       Gaps
  Heinonen K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, Lhe human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).

EMBL; AF363578; AAL50379:1; --
Interpro; IPR09729; BAALC N. 1.

Effect. PF06989; BAALC N. 1.

SEQUENCE 180 AA; 19224 MW; 380183E0F188F684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWIRETESIWLTYIDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                                                                                                                                                  2; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 145;
                                                                                                                                                                                                                                                                                          Score 750.5; DB 2; Length 1
Pred. No. 7.5e-53;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.3%; Score 664; DB 2;
84.1%; Pred. No. 5.5e-46;
iive 12; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVTINVIDSIQOMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EVTINVTESIRQVDRNQRITKKCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                               Query Match 96.5%;
Best Local Similarity 80.6%;
Matches 145; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAALC isoform 1-6-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

Q8VHV1

```
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirozan T., Hirozan T., A Hori P., Imotani K., Ishii Y., Itoh M., Kagawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (ApR-2002) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AK571320, AAL50516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Eprague-Dawley,
MEDLINE-21574584; PubMed=11707601;
MEDLINE-21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
FARGE, the human member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL, AB0731818; BAB70507.1;
EMBL, AB771321, AALSO517.1;
InterPro; IPRO9928; BAALC.N;
FAMP, PRO6989; BAALC.N; 1.
SERQUENCE 145 AA; 15475 MW; DSA27AD67456F341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.4%; Score 649; DB 2; Length 14
83.4%; Pred. No. 8.9e-45;
ive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.9%; Score 645; DB 2; Length 14
83.4%; Pred. No. 1.9e-44;
ive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang X., Tian Q., Li W., Okano A., Suzuki T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF06989; BAALC N; 1.
SEQUENCE 145 AA; 15515 MW; 4972670A618C4D6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Dem-A20-4 (BAALC isoform 1-6-8).
Name=dem-A20-4; Synonyms=Baalc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1928704; Baalc.
InterPro; IPR009728; BAALC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.4
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Simi
Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q920K5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q920K5
               RA
RA
RA
RA
RA
DR
RL
SQ
SQ
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SO DE READ DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SE SO DE SE SE SO DE SE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO DE SO D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
BAALC isoform 1-6-8 (Mus musculus 16 days neonate cerebellum cDNA,
RIKEN full-length enriched library, clone:9630028H16 product:brain and
acute leukemia, cytoplasmic, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINE-20499374; PubMed=11042159;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A., Bloomfield C.D., de la Chapelle A., Is human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/61; TISSUB=Cerebellum;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Fujiwake S., Inoue K., Togawa K., Tanaka T., Ohara E., Watshiki M., Conda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=99279223; PubMed=10349636;
Carninci P., Hayashizari Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                       145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/63; TISSUE=Cerebellum;
The FANTOM Consortium,
                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21574584; PubMed=11707601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] -
SEQUENCE FROM N.A.
STRAIN=129S6/SvEvTac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Name=Baalc
```

ACCOORD BE SEE

ö

Gaps

ö

9 9

```
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                           61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                        MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL 60
            1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS----
                                                                                                                                                                                                                                                                                                                      Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810457D07 product:brain and acute leukemia,
Vytoplasmic, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009728; BAALC N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 149 AA; 15577 MW; DB26C19969B91F6E CRC64;
                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 569.5; DB 2
Pred. No. 2.4e-38;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AA.
                                                                                                   121 EVIINVIDSIQOMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCPNPOSLSSGPLTOKONGLOTTE 109
                                                                                                                                                                                       Created)
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                             MEDLINE=21574584; PubMed=11707601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCPNPQSLSSGPLTQKQNGLQTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 75.7
Matches 109; Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
BAALC 1-5-6-7-8.
                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:14333; BAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 -----
                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                           Q8WXS1;
01-MAR-2002
                                                                                                                                                                                                                                 Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9CYS9
                                                                                                                                                                   Q8WXS1
                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
                                                                                                                                                      OBWXS:
                                                                                                                                                                   DE DE DE DE OX OX OX OX
                    8
                                          ð
                                                                g
                                                                                      ð
                                                                                                          용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Arahimasa K., Akimura T., Arai A., Aono H.,

A Arakawa T., Boro H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AKOll3558; BAB28808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERANDES FROM N.A.
SERANDES STRAINS CSTBLING STRAINS CSTRAINS CSTBLING STRAINS CSTRAINS CSTRAINS CSTRAINS CSTRAINS CSTRAINS CSTBLING THE NUMBER STRAINS STAGE TO STRAINS STAGE TO STRAINS STAGE TO STRAINS STAGE TO STRAINS STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO STAGE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CSTBL/61; TISSUE-Whole body;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKE integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1928704; Baalc.
TRNCE 123 AA; 13391 MW; 33DFCB5F8CFAA0AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 DAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 381; DB 2
Pred. No. 3e-23;
                                                                                                                                                                                                                                 "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Whole body; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.08;
                                                                                                                                                                          Carninci P., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
```

```
and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                           Proc. Natl. Acad.
                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAALC protein.
                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                          54;
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH35038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH35038
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH35038
      à
                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLED 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                            MEDLINE=21574584; PubMed=11707601;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutilas S., Kolitz J.E., Archer K.J.,

MIDLINE=21574584; PubMed and J.L., Leone G., Rush L.J., Proher K.J.,

MIDLINE S., Mill M., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

EMBL, AF361578; AAL50380.1;

Interpro, 1PR009728; BAALC.N.

PERM; PR06999; BAALC.N.

SEQUENCE 73 AA, 7871 MW; 98DBC2E6EEF524A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21574584; PubMed=11707601;
Tanner S.M., Austin U.L., Leoone G., Rush L.J., Plass C., Heinonen K.,
Mrozek K., Sill H., Knuulila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                       39.7%; Score 309; DB 2; Length 73; 96.6%; Pred. No. 1e-17; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last Sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
BAALC isoform 1-8 (BAALC protein) (BAALC 1-8)
                                                                                                                   Last sequence update)
Last annotation update)
Ą
                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                     01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Conservative
                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                              BAALC 1-4-5-6-8.
                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                         Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=BAALC;
                91
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                          OSXMBO
                                                                              OSWASO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8WTP6
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8WXS0
              g
                                                                              à
```

```
**MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Alausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Blat D.B., Strausberg R.L., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H., And Richards S., Worley K.C., Hale S., Garchen G.Y., Gibbs R.A., Fielton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Lakeryinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Shevchind D.K., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Shevchind D.K., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Marra M.A., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A., Touchman J.W., Green E.D., Marra M.B., Touchman J.W., Green E.D., Shevchind J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Sch
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodeegren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anno sapiens (Human).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.,
Strausberg R.,
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF37123; AAH35019.1; -.
EMBL, BC035038; AAH35038.1; -.
EMBL, AF36378; AALS0378.1; -.
InterPro; IPR009728; BAALC_N.
Pfam; PF06998; BAALC_N.
Pfam; PF06998; BAALC_N.
SEQUENCE 54 AA; 5663 MW; FEF0B4EABED9B829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-WAR-2004 (TrEMBLrel. 27, Created) 02-WAR-2004 (TrEMBLrel. 27, Last sequence update) 02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.4%; Score 299; DB 2; I 100.0%; Pred. No. 4.7e-17; tive 0; Mismatches 0;
```

.. 0

ö

```
InterPro; IPR009728; BAALC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 94.4%;
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20,
26,
                                                                                                     Similarity 94.4%; 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%;
                                                                                                                                                                                                                                                                                                                                                             27,
                                                                                                                                                                                                                                                                                                                                                                                 -2004 (TrEMBLrel. 27,
                                                                                 36.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBI
05-JUL-2004 (TrEMBI
BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Baalc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Baalc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                         Q790N3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VBS8
                                                                                                                                                                                                                                                                                                                        Q790N3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
Q8VBS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                              Matchea
                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                               Q790N3
                                                                                                                                                                                                                                                                                                                        JOSEPH SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOR
                                                                                                                                                                                                             d
                                                                                                                                                                        ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]

SEQUENCE FROM N.A.

MEDLINE=21574584; PubMed=11707601;

MEDLINE=21574584; PubMed=11707601;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuttla S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

"NATI. Acad. Sci. U.S.A. 98:13901-13906 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                    Gaps
                                                                                                                                                                                         54
                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                    1 MGCGGSRADALEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL; AF365578; AAL50382.1; -.
InterPro; IPR009728; BAALC_N.
Pfam; PF06989; BAALC_N.
SEQUENCE 80 AA, 8573 MW; 70BE9B91C3245E2D CRC64;
                                                                                                            Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 293; DB 2; Length 80; Pred. No. 2.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                  Indels
  Strausberg R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO35038; AAH35538.1; -.
SEQUENCE 54 AA; 5663 MW; PEF0B4EABED9B829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                    ö
                                                                                                                                4.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.7%; Scor.
100.0%; Pred. No. a...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                              80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 AA
                                                                                                        38.4%; Score 299; DB 100.0%; Pred. No. 4.74 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                            38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Conservative
                                                                                                                              Best Local Similarity 100.0
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=BAALC;
Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=BAALC;
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D8WNE8;
                                                                                                                                                                                                                                                                                                                                                Q8WXS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O8WNE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE
                                                                                                                                                                                                à
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
```

```
MEDLINE-Sprague-Dawley;
MEDLINE-215/4584; PubMed=11707601;
MIDLINE-215/4584; PubMed=11707601;
MIDLINE-215/4584; PubMed=11707601;
MIDLINE-215/4584; PubMed=11707601;
MIDLINE-215/4584; PubMed=11707601;
MIDLINE-215/4584; PubMed=11707601;
MIDLINE A., Bloomfield C.D., de la Chapelle A.;
MIDLINE A., Bloomfield C.D., de la Chapelle A.;
MIDLINE A., Bloomfield C.D., de la Chapelle A.;
MIDLINE A., Bloomfield C.D., de la Chapelle A.;
MIDLINE A., Bloomfield C.D., de la Chapelle A.;
MIDLINE A., BRAIL A., BRAIL A., BRAIL A., BRAIL A., BAALC. N., I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
STRAIN=12956/SvEvTac.
STRAIN=12956/SvEvTac.
STRAIN=12956/SvEvTac.
STRAIN=12956/SvEvTac.
STRAIN=12956/SvEvTac.
Table S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mamalian neuroectoderm gene lineage, is implicated in hematopoisesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                     1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSNAAPDSGPEAGGLQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGCGGSRADAIEPRYYESWTRETESTWLIYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                       .;
0
                                                                                             DB 2; Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 54;
                                                                                       Score 282; DB 2; Length 54
Pred. No. 1.1e-15;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
Pfam; PF06989; BAALC_N; 1.7
SEQUENCE 54 AA; 5681 MW; 6538C3DABED9B825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 AA; 5667 MW; FEE8COEBFBCDB829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 278; DB 2;
Pred. No. 2.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
```

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                   01-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNA-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
SI:&C215113.3 (Novel protein similar to human brain and acute
leukemia, cytoplasmic (BAALC)) (Fragment).
Name=SI:&C215113.3;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWIRETESTWLIYIDSDALPSAAAIDSGPEAGGLHAG 54
                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                  Query Match 35.7%; Score 278; DB 2; Length 54; Best Local Similarity 94.4%; Pred. No. 2.3e-15; Matches 51; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
20.7%; Score 161; DB 2; Length 32;
Best Local Similarity 90.6%; Pred. No. 3.4e-06;
Matches 29; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] _
SEQUENCE FROM N.A.
Sehra H.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL807244; CAD87801.1; -
InterPro; IPR0928; BAALC_N.
Pfan; PP6989; BAALC_N, 1.
NON TER
SEQUENCE 32 AA; 3663 MW; 916AS445D263B7F7 CRC64;
              MGD; MGI:1928704; Baalc.
Interpro; IRR009728; BAALC.N.
Pfam; PP06989; BAALC N; I.C.
SEQUENCE 54 AA; 5667 MW; FEE8COEBFBCDB829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTD 32
                                                                                                                                                                                                                                                                                                   32 AA.
                                                                                                                                                                                                                                                                                                 PRT;
EMBL; AF371324; AAL50520.1; -.
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                            SARBS
                                                                                                                                                                        ò
                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

1 MGCGGSRADAIEPRYQESWTRETESTWLTNTE 32

Search completed: November 17, 2004, 15:27:50 Job time : 108.667 secs

us-10-705-716a-8.rup

ŧ

```
November 17, 2004, 14:59:59; Search time 103.667 Seconds (without alignments) 804.784 Million cell updates/sec
5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
                                                                  using sw model
                                                                                                                                                                US-10-705-716A-8
767
                                                                  - protein search,
                                                                                                                                                                   Title:
Perfect score:
                                                                  OM protein
                                                                                                    Run on:
```

1 MGCGGSRADAIEPRYYESWT.......VTENIRQMDRSKRVTKNCIN 145 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: uniprot\_sprot:\* 2: uniprot\_trembl:\* UniProt 02:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# CIMMADIES

RIES	Description	O844N mnscn1n	Q920k5 rattus norv	Q9ha93 homo sapien		Q8wxs3 homo sapien		Q8wxs1 homo sapien		Q8vbs8 mus musculu	Q8wxs0 homo sapien	Q8wtp6 homo sapien		Q8wxs2 homo sapien		Q801v5				013412 asperg	6 Caa68196 aspergill	Q7k2p9 drosophila			Q83h42 tropheryma	Q83ny7 tropheryma	Q9vy16 drosophila	9 Aaf48389 drosophil	Q9fnv4 porphyra ye		AVS P25242 sugarcane m	***************************************
SUMMARIES	ΩI	Q8VHV1	Q920K5	Q9HA93	Q8WNE9	Q8WXS3	Q9CYS9	Q8WXS1	Q790N3	Q8VBS8	08WW80	O8WTP6	AAH35038	Q8WXS2	Q8WNE8	Q801V5	PVDA PLAKN	Q7XPB1	Q8W0A0	AREA ASPNG	CAA68196	Q7K2P9	Q8IR46	Q961T1	Q83H42	Q83NY7	Q9VY16	AAF48389	<b>Q9FNV4</b>	066155	POLG SUMVS	00.00
	DB	2	~	~	N	~	N	N	7	~	N	~	~	~	~	~	Н	~	~	Н	~	ď	~	~	7	~	~	7	7	7	-1	•
	Length	145	145	145	145	180	123	149	54	54	73	54	54	80	54	32	1073	1449	178	882	882		494		591	591	629	629	773	253	365	
d	Query Match	100.0	97.3	84.6	82.7	81.0	62.6		38.3	38.3	37.5	36.2	36.2	35.5	34.8	21.0	11.4	11.2	11.1	11.1	11.1	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	,
	Score	767	746	649	634	621.5	480	472.5	294	294	288	278	278	272	267	161	87.5	86	85.5	82	85	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84	84	
	້ ຜ		2	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	ŗ

Q871v5 neurospora Q92269 penicillium	Q7pvsl anopheles g Q7uz29 rhodopirell	Olasola penicilium Olate leucophaea	Q911a3 white spot Q82ay5 streptomyce	Q91tq3 tupaia herp 074641 aspergillus	P50494 plasmodium	Aag92950 plasmodiu	060341 homo sapien
Q871V5 NRFA_PENUR	Q7PVS1 Q7UZ29	AREA PENRO QBMTC2	Q91LA3 Q82AY5	Q91TQ3 074641	PVDG PLAKN	AAQ92950	AOF2_HUMAN
7 7	00	40	0 0	0 0	٦,	10	٦
291 865	476 585	214	1100 219	228 516	1070	155	852
10.9	10.8	10.8	10.6	10.6	10.6	10.5	10.5
83.5 83.5	83	83 81.5	81.5 81	81 81	81	80.5	80.5
33	35	37	8 6 8 6	40	4.2	44	45

## ALIGNMENTS

```
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
BAALC isoform 1-6-8 (Mus musculus 16 days neonate cerebellum CDNA, RIKEN full-length enriched library, clone:8630028H16 product:brain and acute leukemia, cytoplasmic, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=20499374; PubMed=11042159;
Garninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C., Heinonen K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la chapelle A.; Caligiuri M.A., Bloomfield C.D., de la chapelle A.; EAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=9279253; Pubmed=10349636;
MEDLINGI P., Hayashizak; Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                         145 AA.
                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Cerebellum;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851;
                                                                     PRT;
                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2004 (TrEMBLrel. 28,
                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=129S6/SvEvTac;
                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                         Name=Baalc
                                                                                                       Q8VHV1;
                                                                         Q8VHV1
RESULT 1
                                      RAPER REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION OF THE REPRESENTATION O
```

Heinonen K.,

ö

Gaps

ö

9

```
SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SSNGVLRPAAPGGIANPEKKWNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE AMOLE GENDIYO;

PubMed=14702039;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Ramamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

A Murakami K., Yasuda T., Iwayanagi T., Wadatsum M., Shiratori A.,

Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

Ninomiya K., Ishibashi T., Yamashi H., Murakawa K., Fujimori K.,

Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

Non Y., Takiguchi S., Watanabe S., Yosida M., Hotuca T., Kusano J.,

Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

Kanehori K., Takahashi-Pujii A., Hara H., Tanase T., Kusano J.,

Kanehori K., Matsunawa H., Ichihara T., Shiohata N.,

Noshikawa Y., Matsunabe T., Sugiyama A., Takemoto M., Kawakami B.,

Noshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,

Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Pujiwara T.,

No T., Yamada K., Kujii Y., Ozaki K., Hirao M., Ohmori Y.,

Rawabata A., Hikiji Y., Ozaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji Y., Ozaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji Y., Ozaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji Y., Osaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji Y., Osaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji Y., Obaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji Y., Obaki K., Hirao M., Ohmori Y.,

Kawabata A., Hikiji T., Robata K., Kulo M.,

Kawabata A., Hikiji T., Robata K., Kulo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein FLJ12015 (BAALC isoform 1-6-8) (Brain and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                            Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., Kolitz J.B., Archer K.J., Caligiut M.A., Bloomfield C.D., de la Chapelle A.; Gristli M.A., Bloomfield C.D., de la Chapelle A.; Lineade, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; EMBL, AB073318; BAB705071; -. EMBL, AR371321, AAL505171; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.3%; Score 746; DB 2; Length 145; 97.2%; Pred. No. 2e-62; rive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR009728; BAALC N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 145 AA; 15475 MW; D5A27AD67456F341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EVAISVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukemia, cytoplasmic) (BAALC 1-6-8)
Name=BAALC;
                                        STRAIN=Sprague-Dawley;
MEDLINE=21574584; PubMed=11707601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Whole embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9HA93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9HA93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HA93
    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKEMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CSTBL/60; TISSUE-Cerebellum;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Alzawa K., Akimura T., Hara A., Hashizuwa W.,
Hayashida K., Hayatsu N., Hanagaki T., Hara A., Hashizuwa T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (Appr-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SSNGVLRPAAPGGIANPEKKANCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                        STRAIN-C57BL/64) TISSUE-Cerebellum;
MEDLINE=2050913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa T., Nakamura S., Hazama M., Nishiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Tozawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang X., Tian Q., Li W., Okano A., Suzuki T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPR009728; BAALC N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 145 AA; I5515 MW; 4972670A618C4D6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 767; DB 2;
100.0%; Pred. No. 2.1e-64;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FINITED STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0920X5,
01-DEC-2001 (TrEWBLrel. 19, Created)
01-DEC-2001 (TrEWBLrel. 19, Last seq
05-JUL-2004 (TrEWBLrel. 27, Last ann
Dem-A20-4 (BAALC isoform 1-6-8)
Name-dem-A20-4; Synonyms-Baalc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF371320; AAL50516.1; -. EMBL; AK079337; BAC37611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 145, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1928704; Baalc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q920K5
```

à g 8 a ð 셤 Okamoto S.,

145 AA.

PRT;

PRELIMINARY;

```
CHISOLOGY TESUBERSTAY, PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausberg R.L., Feingold E.A., Grouse L.H., Schuler G.D.,

Klausber R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Alschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.H., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.H., Hong L.,

Brapleton M., Soares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

R. Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Krzywinski M.J., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

RA Krzywinski M.N., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

RGeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SSNGVIRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Makagawa K., Mizushima-Sugano J., Satoh T., Shiral Y., Takhashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                        MEDLINE=21574584; PubMed=11707601; Rush L.J., Plass C., Heinonen Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomiteld C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF363578; AAL50377.1; -.
INCEPPC, IPR009728; BAALC N.
Pfam; PF06989; BAALC N; 1.
SEQUENCE 145 AA; 15551 MW; CFB92BBE283DD92E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 649; DB 2;
; Pred. No. 2.8e-53;
10; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || ||||::|:|||||:|
EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK022077; BAB13960.1; -. EMBL; AF371319; AAL50515.1; -. EMBL; BC011517; AAH11517.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.6%;
Best Local Similarity 83.4%;
Matches 121; Conservative 1
                                                                                                                                                              Nat. Genet. 36:40-45(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                       rissuE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SSNGVLRPAAPGGIANPEKKVNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGCGGSRADALEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSNAAPDSGPEAGGLQAGVLEDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; Engaluri M.A., Bloomfield C.D., de la Chapelle A.; Ender human member of a novel mammalian neuroectoderm gene proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).

EMBL, AF363578, AALS0379.1, -
Interpro; IPR009728; BAALC_N.

Pfam; PR06899; BAALC_N.

SEQUENCE 180 AA; 19224 MW; 380183E0F188F684 CRC64;
                                                                                                                                                                                                                                                                                                                                       MEDLINE=21574584; PubMed=11707601;
MEDLINE=21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
Tanner human member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL, AF371322; AAL50518.1;
ThterPro, IPROF0928; BALC_N.
Pfam; PRO6999; BALC_N.
Pfam; PRO6999; BALC_N.
Pfam; PROG0998; BALC_N.
Pfam; PROGUENCE 145 AA, 15401 MW; C75ED7D00EF82E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.0%; Score 621.5; DB 2;
67.2%; Pred. No. 1.4e-50;
ive 10; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.7%; Score 634; DB 2;
82.1%; Pred. No. 7.3e-52;
ive 11; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 EVIINVTESIRQVDRNQRITKKCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21574584; PubMed=11707601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                       20,
20,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 82.1
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                             01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                            BAALC isoform 1-6-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 121; Conserv
                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                         MCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAALC 1-5-6-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=BAALC;
                                                                                                                                                                        Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WXS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8WXS3
                                 OBWNE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8WXS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS SO OS 
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

ä

RESULT 4 OBWNE9

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEXM8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8WXS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8WXS1
                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                          61 KIKAPTDSVSDEGLFSASKWAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                86 OCPNSONLSSGPLTOKONGLWATEAKRDAKRMSAREVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                          9
                53
  MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-----
                            MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                ----GVLEDGLSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810457D07 product:brain and acute leukemia,
cytoplasmic, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTRAIN-C57BL/61; TISSUE-Whole body;
MEDLINE-2050913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Sonno H., Alzawa K., Nakamura S., Hazama M., Nishine T., Tashiro H., Itoh M.,
Yamamoto R., Matsumuto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki M.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                     123 AA.
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; Pubmed=11217851;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Baalc;
                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                   Q9CYS9;
                                                                                                                                                                                                                                                                                                                                           Q9CYS9
                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                 Q9CYS9
                                          g
                                                                                         à
                                                                                                                               g
                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                              AC PER SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE
ò
                                                                                                                                                                                                                        d
```

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 AGVLEDGLSSNGVLRPAAPGGIANPEKKNNCGTQCPNSQNLSSGPLTQKQNGLWATEAKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KIKAPTDSVSDEGLFSASKWAPLAVFSHGMLEBGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-whole body;
Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kabukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yammura T., Yasunishi A., Yoshido M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 SGVLEDGLSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GVLEDGLSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MCCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-21574584; PubMed=11707601;

MEDLINE-21574584; PubMed=11707601;

Manner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knutila S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.,

"BAALC, the human member of a novel mammalian neuroectoderm gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.6%; Score 472.5; DB 2; Length 149; 65.3%; Pred. No. 1.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                         Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK013358; BAB28808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               123 AA; 13391 MW; 33DFCB5F8CFAA0AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AA; 15577 MW; DB26C19969B91F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 DAKRMSAREVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.6%; Score 480; DB 2; 98.9%; Pred. No. 2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCPNSQNLSSGPLTQKQNGLWATE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:14333; BAALC.
InterPro; IPR009728; BAALC.N.
Pfam; PF06989; BAALC N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1928704; Baalc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAALC 1-5-6-7-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

54 54

121

\$5,000 to

SO OR SO OR

Q790N3

œ RESULT

2790N3

```
1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLED 58
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21574584; PubMed=11707601; MEDLINE-21574584; PubMed=11707601; MEDLINE-21574584; PubMed=11707601; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuttila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; Manan member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL, PR363578; ALLS0380.1; -
InterPro; IPR009728; BAALC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDDLINE-21574584; PubMed=11707601;
MEDDLINE-21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
Mrozek K., Sill H., Knuttila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 288; DB 2; Length 73
Pred. No. 1.4e-19;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7871 MW; 98DBC2E6E6EF524A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last amnotation update)
BAALC isoform 1-8 (BAALC protein) (BAALC 1-8).
                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AA
                                                                                                                                                                 Ź
                                                                                                                                                              73
                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%;
91.4%;
                                                                                                                                                                                                       20,
20,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 AA;
                                                                                                                                                                                                                                                                     BAALC 1-4-5-6-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=BAALC;
                                                                                                                                                                                                                                                                                       Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                    Q8WXS0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBWTP6;
                                                                                                                                                                 Q8WXS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8WTP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                        RESULT 10
                                                                                                                                             Q8WXS0
                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                       g
                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley;
MEDLINE=21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
Mrozek K., Sill H., Knutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21574584; PubMed=11707601; MEDLINE-21574584; PubMed=11707601; Tanner S.M. Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mill H., Knuttia S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammallan neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lineage, is implicated in hematopoissis and acute leukemia.", Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL; AF371325; AAL50521.1; -.
InterPro; IPR009728; BAALC.N.
Pfam; PF06899; BAALC.N.
SEQUENCE 54 AA; 5667 MW; FEB8COEBFBCDB829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.3%; Score 294; DB 2; Length 54; 100.0%; Pred. No. 2.6e-20; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEE8COEBFBCDB829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.3%; Score 294; DB 2; L 100.0%; Pred. No. 2.6e-20; tive 0; Mismatches 0;
                                                                                                                            54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 AA
Created)
                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR009728; BAALC_N. Pfam; PF06989; BAALC_N; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                 Best Local Similarity 100.
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1928704; Baalc
                                                                                                                                                                                                                           BAALC isoform 1-8.
Name=Baalc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
```

Query Match

Local

Matches

Name=Baalc;

SAVBC QBVBSB

RESULT 9

g ò

Q8VBS8

SEQUENCE Query Match

ö

0; Gaps

ô

```
SEQUENCE FROM N.A.
                 SEE
                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HODE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toophiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.A.,
Touches S.J., Marra M.J.,
Touches S.J., Marra M.J.,
Touches S.J., Marra M.J.,
Touches S.J., Marra M.J.,
Touches S.J., Marra M.J.,
Touches S.J., Marra M.J.,
Touches S.J., Marra M.J.,
Touche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Eromnstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Srankod J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGCGGSRADAIEPRYYESWIRETESTWLIYIDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 278; DB 2; Length 54;
Pred. No. 8.5e-19;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (dVIL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AR31519.1; EMBL; BC035038; AAH35038.1; -... EMBL; AF365578; AAH35038.1; -... EMBL; AF365578; AAL50378.1; -... EMBL; PP06698; BAALC_N. PP0698; BAALC_N. T. PP0698; BAALC_N. 1... PP088.5 BAALC_N. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use cDNA sequences.";
Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH35038;
02-MAR-2004 (TYEMBLES). 27,
02-MAR-2004 (TYEMBLES). 27,
02-MAR-2004 (TYEMBLES). 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAALC protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH35038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH35038
          ð
```

```
MEDLINE=21574884; PubMed=11707601;
MEDLINE=21574884; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoissis and acute leukemia.";
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL, AF304579; AALSO392.1;
InterPro; IPRO9728; BAALC.
Pfam: PF06989; BAALC N; 1.
SEQUENCE 80 AA; 8573 MW; 70BE9B91C3245E2D CRC64;
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21574584; PubMed=11707601;
Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Prozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
Caligiuri M.A., Bloomicield C.D., de la Chapelle A.;
"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Cetartiodactyla, Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWIRETESTWLIYYDSDAPPSAAAPDSGEAGGLHSG
                                                                                                                                                                                                            1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGCGGSRADA1EPRYYESWTRETESTWLTYTDSDAPPSAAADDGGPEAGGLHS
                                                                                                                               Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 80;
                                                                                                                        Score 278; DB 2; Length 54
Pred. No. 8.5e-19;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                           EMBL/GenBank/DDBJ databases.
                                                            EMBL; BC035038; AAH35038.1; -. SEQUENCE 54 AA; 5663 MW; FEF0B4EABED9B829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 272; DB 2
Pred. No. 5e-18;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
TISSUE=Brain,
Strausberg R.;
Submitted (JUL-2002) to the
                                                                                                                             36.2%;
                                                                                                                                            l Similarity 94.4%;
51, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20,
20,
26,
                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Conservative
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel. BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                          Query Match
Best Local Similarity
Matches 51, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                              Q8WXS2;
                                                                                                                                                                                                                                                                                                                                                         Q8WXS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8WNE8
                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
```

. 0 1

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
S1:zC215113.3 (Novel protein similar to human brain and acute
leukemia, cytoplasmic (BAALC)) (Fragment).
Name=S1:zC215113.3;
Name=S1:zC215113.3;
Name=S1:ZC215113.3;
Sachinoteryotis Metazoa; Chordata; Caniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCB1_Tax1D=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                             .
0
                                                                                                                          Query Match 34.8%; Score 267; DB 2; Length 54; Best Local Similarity 92.6%; Pred. No. 9.3e-18; Matches 50; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.0%; Score 161; DB 2; Length 32; 90.6%; Pred. No. 5e-08; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AL807244; CAD87801.1; -.
InterPro; IPR009728; BAALC_N.
Pfam; PF06989; BAALC_N, 1.
NON_TER 3.2
SEQUENCE 32 AA; 3663 MW; 916A5445D263B7F7 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
EMBL; AF371326; AAL50522.1; -
Interpro; IPR009728; BAALC_N.
Pfam; PR06989; BAALC N; 1.
SEQUENCE 54 AA, 5681 MW; 6538C3DABED9B825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   32 AA.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.6
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sehra H.;
                                                                                                                                                                                                                                                                                                                                                              Q801V5
Q801V5;
                                                                                                                                                                                                                                                                                                                      RESULT 15
0801V8
AC 0801V
AC 0801V
DT 01-JU
DT 01-JU
DT 01-ME
DE SI:ZC
DE SI:ZC
DE REACH
OC EUKAR
OC CYPTI
OX NCEI
RN (1)
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
RR SEQUE
    3 K K K K K
                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                     g
```

Search completed: November 17, 2004, 15:27:52 Job time : 105,667 secs

ව ව